

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACCGCGTCCGGGCGGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTCGTCTCCCG
CAGCGCTACCCGCCATGCGCCTGCCGCCGGCGCTGGGCTCCTGCCGCTTGCTG
CTGCTGCCGCCGCCGGAGGGCCAAGAAGCCAGGCCACCGAAAGAAGAACCTTGCGGGAGAAC
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCTGCTGGAGATC
CTGGAGGGCTGTGCGAGAGCAGCGACTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCCTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCGACTGTCTCGCATGC
CAGGGCGGATCCAGAGGCCCTGCAGCGGAATGGCCACTGCAGCGGAGATGGAGACAGACA
GGGCGACGGGTCCGTGCCGACATGGGTACCAGGGCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGCCTGACCAACAGAGACTGCAGCGAGTGTGAAGTGGCTGGGTGCT
GGACGAGGGCGCCTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTG
GGCTGCACAGGGGAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA
CGGACAGTGTGCAGATGTGGACGAGTGCCTACTAGCAGAAAAAACCTGTGTGAGGAAAAACG
AAAATGCTACAATACTCCAGGGAGCTACGTCTGTGTGCTGCAGGCTTCGAAGAACG
GAAGATGCCTGTGCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCGACACAGCT
GCCCTCCCGCGAAGACCTGTAATTGTGCCGACTTACCCCTAAATTATTCAAGAAGGATGTCC
CGTGGAAAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTGTCCTTAAACAGCTGCATTCTTGGTTGTTCTTA
AACAGACTTGTATATTTGATACAGTTCTTGTAAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAAAGGGCGGCCGACTCTAGAGTCGACCTGCAGAAGC
TTGGCCGCCATGGCCAATTGTTATTGCAGCTTACGATTGTTACAAATAAGCAATAGCA
TCACAAATTTCACAAATAAGCATTTCAGCTGATTCTAGTTGTGGTTGTCCAAACTC
ATCAATGTATCTTATCATGTCTGGATCGGAATTAAATTGCCGCGCAGCACCATGGCCTGAAAT
AACCTCTGAAAGAGGAACTTGGTTAGGTACCTCTGAGGCGAAAGAACCAAGCTGTGGAATG
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCAGTGC
ATCTCAATTAGTCAGCAACCCAGTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLPIIIIIIPPAPEAKKPTPCHRGRGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIRL
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKCCSPGTYPDCLACQGGSQRPCSG
NGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNETHSICTACDESCKTCGLTNRDCGECEVGWLDE
GACVDVDECAAEPPPCSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKT
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCAAGTGCACCTCGGTTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACCGCGTCCGCCAGGCCAGGGCAGCGGCCAGCGTCTAAACGGGAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGGCCAGGTTGCGTAGGTGCG
GCACGAGGAGTTTCCCGCAGCGAGGAGGTCTGAGCAGCAGCATGGCCCGGAGGAGCGCCTT
CCTGCCGCCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGGACTGCCGGCGGAGGC
CGGGCCGCCGAGGAGGAGGCCGTACCTATGGATCGATGCTCACCAAGGAAGAGTACTCA
TAGGATTGAAGAAGATATCCTGATTGTTAGAGGGAAAATGGCACCTTACACATGAT
TTCAGAAAAGCGAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTCAC
CTGGCAAGCTGCAGGGCAGGCAGAAATACTTCTATGAATTCTGCTTGCCTCCCTGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGTCCTCTGCTGGAAACAGTGCCTCACAGGCA
TCAGTTGTTCAAGTGGTTCCCATGCTTGAAAACAGGATGGGTTGGCAGCATTGAAGT
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCAAACACCTCAAATGCTATCT
TCTTTAAACATGTCAACAAGCTGAGTGCCAGGGGGTGGCAAATGGAGGTTTGTAAAT
GAAAGACGCATCTGCAGTGTCTGATGGTTCCACGGACCTCACTGTGAGAAAGCCCTTG
TACCCACGATGTATGAATGGTGGACTTGTGACTCCTGGTTCTGCATCTGCCAACCTG
GATTCTATGGAGTGAACGTGACAAAGCAAACGCTCAACCACCTGCTTAAATGGAGGGACC
TGTTCTACCTGGAAATGTATTGCCCTCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAATGCCACACCCCTGCGAAATGGAGGTAAATGCATTGGTAAAGCAAATGTAAGTGT
CCAAAGGTTACCAAGGGAGACCTCTGTCGAAAGCCTGTCTGCCAGCCTGGCTGGTGACAT
GGAACCTGCCATGAACCCAAACAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA
TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGGCCAGCTCAGGCAGC
ACACGCCCTCACTAAAAAGGCCAGGAGCGGGGATCCACCTGAATCCAATTACATCTGG
TGAACTCCGACATCTGAAACGTTTAAGTTACACCAAGTTCATGCCCTTGTAAACCTTCA
TGTGTTGAATGTTCAAATAATGTCATTACACTTAAGAATACTGCCCTGAATTATTAGCT
TCATTATAAAATCACTGAGCTGATATTACTCTCCCTTAAAGTTCTAAGTACGTCTGTAG
CATGATGGTATAGATTTCTGTTCACTGCTTGGACAGATTATATTATGTCAATTGA
TCAGGTTAAAATTTCAGTGTGAGTGGCAGATATTCAAAATTACAATGCATTATGGT
GTCTGGGGCAGGGAAACATCAGAAAGGTTAAATTGGCAAAATGCGTAAGTCACAAGAAT
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTCAAGATTATTGTCAGATATTAGAT
GTTTGTACATTAAAATTGCTCTTAATTAAACTCTCAATACAATATATTGACC
TTACCAATTATCCAGAGATTCACTGATTAAAAAAATTACACTGTGGTAGTGGCATT
AAACAATATAATATTCTAAACACAATGAAATAGGGAAATAATGTATGAACCTTTGCAT
TGGCTTGAAGCAATATAATATTGTAACAAAACACAGCTCTTACCTAATAAACATT
ACTGTTGTATGTTAAAGGTGCTGCTTGTAGTTGGAAAAA
AAAAAAAAAAAAAAAAAAGGGCGGCCGACTCTAGAGTCGACCTGCAGAAGCTGGC
CGCCATGGCCCAACTTGTATTGCAAGCTATAATG

FIGURE 4

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVNVPPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGPHECEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKICPPGLEGEQCEISKCPQPCRNGGKCIKGSKCKCSKGYQGDLCSKPVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDP
• PESNYIW
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Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGGCGTGGCGTCCGGCGTCCGAGAGCCAGGAGGGCGAGGGCGCGGGCCAGCCCTGGG
CCCCAGCCCACACCTTCAACCAGGGCCCAGGAGCCACCATGTGGCGATGTCCACTGGGGCTAC
TGCTGTTGCTGCCGCTGGCTGGCACTTGGCTCTGGGTGCCAGCAGGGTCGTGGCGCCGG
GAGCTAGCACCAGGTCTGCACCTGCGGGCATCCGGGACCGGGAGGCCGTACTGCCAGGA
GCAGGACCTGTGCTGCCCGGGCGTCCGACGACTGTGCCCTGCCCTACCTGGCGCCATCT
GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC
TGCCTCGGCGTGCACCCCCCTTTCCCCGATCCAAGGATGTATGCATGGAGGTGCTATCTA
TCCAGTCTTGGGAACGTACTGGACAACGTAACTGTAACCGTTGCACCTGCCAGGAGAACAGGCAGT
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
GAACCACAGCGCCTCTGGGCATGACCCGGATTGAGGGCATTGCTACCGCCTGGCACCA
TCCGCCATCTCCTCGGTATGAACATGCATGAAATTATACAGTGTGAACCCAGGGAG
GTGCTTCCCACAGCCTCGAGGCCTCTGAGAAGTGGCCAACCTGATTGATGAGCCTCTTGA
CCAAGGCAACTGTGCAGGCTCTGGCCTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
CAATCCATTCTCTGGGACACATGACGCCGTGTCCTGCCCCAGAACCTGCTGTCTTGAC
ACCCACCAAGCAGCAGGGCTGCCCGGTGGCGTCTCGATGGTGCCTGGTGGTCTCGTGC
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTCTCGGGCCGTGAACGAGACGAGGCTGGCC
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGCAAGCGCCAGGCCACTGCC
CACTGCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTACTCCTGTCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAAATGCCCTGTCCAAGCCCTCA
TGGAGGTGCATGAGGACTTCTTCTATAACAAGGGAGGCATCTACAGCCACACGCCAGTGAGC
CTTGGGAGGCCAGAGAGATAACGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCCGCAACTCCTGGGCC
CAGCCTGGGCGAGAGGGGCCACTCCGCATCGCGCCGTCAATGAGTGCACATCGAG
AGCTTCTGCTGGCGTCTGGGCCGTGGCATGGAGACATGGTCATCACTGAGGCTG
CGGGCACCACGCCGGTCCGGCTGGATCCAGGCTAAGGCCGGGAAGAGGCCCAATG
GGCGGTGACCCAGCCTGCCGACAGAGCCGGCGCAGGCCGCCAGGGCGCTAAT
CCCGCGCGGGTTCCGCTGACGCAGGCCCGCCTGGAGGCCGCCAGGGCGAGACTGGCG
GAGCCCCAGACCTCCCAGTGGGACGGGCAGGGCTGGCTGGAAAGAGCACAGCTGCAG
ATCCCAGGCCCTGGCGCCCCACTCAAGACTACCAAAAGCAGGACACCTCAAGTCTCCAGC
CCCAATACCCACCCAAATCCGTATTCTTTTTTTTTAGACAGGGCTTGCTCCG
TTGCCAGGTTGGAGTGCACTGGCCATCAGGCTCACTGTAACCTCCGACTCCTGGTTCA
AGTACCCCTCCACCTCAGCCTCTCAAGTAGCTGGACTACAGGTGCAACCACACCTGGC
TAATTGGTATTTGAAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTGAACT
CCTGGGCTCAAGCGGTCCACCTGCCTCCGCTCCCAAAGTGTGGATTGAGGCATGAGCC
ACTGCACCCAGCCCTGTATTCTTATTCTCAGATATTATTTCTTCACTGTTAAAAA
TAAACCAAAAGTATTGATAAAAAAAA

FIGURE 6

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLLCRGRADDC
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPPFPPPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEQRLLGHDPG
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N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCCTGGCCCTTTCCACAGCAAGCTTNTGCNATCCGATTGTTGCTCAAATCCA
ATTCTCTGGGACACATNACGCCTGTCCTTNGCCCCAGAACCTGCTGTCTTGTACACCCAC
CAGCAGCAGGGCTGCCGCGNTGGCGTCTCGATGGTGCCTGGTGGTCTGCGTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTCTGGGCCGTGAACGAGACGAGGCTGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGCAAGCGCCAGGCCACTGCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAAGGTCACTCCTGTCTACGCCCTCGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGCCCTGTCCAAGCCCTATGGAGG
TGCATGAGGACTTCTTCTATAACAAGGGAGGCATCTACAGCCACAGCCAGTGAGCCTGGG
AGGCCAGAGAGATAACGCCGGCATGGACCCACTCAG

FIGURE 8

GCTGCTTGCCTGTTGATGGCAGGCTGGCCCTGCAGCCAGGCAGTGCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACCGCGCGATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTGAACTGCGTGGATGACTCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCATCCTT
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGGACCCGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTGGTCCCCCAGGCCCTGTGCCACTCCTCACAGACCTG
GCCCAAGTGGGAGCCTGTCCTGGTTCCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCACCCCTGACCCCTCCATGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCTCCAACCCCTCTGCTGCTGTTTC
CATGGCCCAGCATTCTCCACCCCTAACCCCTGTGCTCAGGCACCTCTCCCCCAGGAAGCCTT
CCCTGCCACCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTCCCCCGACCCAGCA
GGGGACAGGCACTCAGGAGGGCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA
GGACAAGAGTCGACGTGAGTTCCCTGGAGTCTCCAGAGATGGGGCCTGGAGGCCTGGAGGAA
GGGGCCAGGCCTCACATTGTCGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAA

FIGURE 9

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSDPASYRLWGAPLQPT
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPPMALSRTPTRQISSDT
DPPADGPSNPLCCCFHGPFAFSTLNPVLRHIFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

FIGURE 10

CCCACCGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCGCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACACTCAGTACGTGAGGGACCAGGGGCCATGACC
GACCAGCTGAGCAGGCGGCAGATCCCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTCAGGTCACCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTGCCAAGC
TCATAGTGGAGACGGACACGTTGGCAGCCGGGTTCGCATCAAAGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGCCCAGCGGGAAAGAGCAAAGACTG
CGTGTTCACGGAGATCGTGTGGAGAACAACTATACGGCCTTCCAGAACGCCGGCACGAGG
GCTGGTTCATGGCCTTCACGCGGCAGGGCGGCCCGCCAGGCTTCCGCAGCCGCCAGAAC
CAGCGCGAGGCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTCCCCAACCACGC
CGAGAACAGAACAGCAGTTGAGTTGTGGCTCCGCCAACCGCCGGACCAAGCGCACAC
GGCGGCCAGGCCCTCACGTAGTCTGGGAGGCAGGGGGCAGCAGCCCTGGGCCCTCCC
CACCCCTTCCCTTCTTAATCCAAGGACTGGCTGGGTGGCGGGAGGGGAGCCAGATCCCC
GAGGGAGGACCCCTGAGGGCCCGAAGCATCCGAGCCCCCAGCTGGGAAGGGGAGGCCGGTG
CCCCAGGGCGGCTGGCACAGTGCCCTTCCCGACGGTGGCAGGCCCTGGAGAGGAAC
GAGTGTCAACCTGATCTCAGGCCACCAGCCTCTGCCGCCCTCCAGCCGGCTCCTGAAGCC
CGCTGAAAGGTCAAGCAGTGAAGGCCTTGCAGACAACCGTCTGGAGGTGGCTGTCTCAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCTCAGCCCCAACCTCCCTGGCTAGACTGTA
GGAAGGGACTTTGTTGTTGTTGTTCAAGGAAAAAGAAAGGGAGAGAGAGGAAATAG
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCACCCCCAACTCCCAGCCC
CGGAATAAAACCATTTCCTGC

FIGURE 11

MGAARLLPNLTLCQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPSGKSKDGVFTEIVLE
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQQQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTCGACATGGAG
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTAC
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTCTGGACTTCACAGAGAACCCATCCAGT
CATTTGATTTGCTGTTATTTTTCTTTTCCACACATTGTATTTAT
TTCCGTACTTCAGAAATGGGCTACAGACCAAAAGTGGCCAGCCATGGGCTTTTCCT
GAAGTCTTGGCTTATCATTCCCTGGGCTACTCACAGGTGTCCAAACTCCTGGCTGCC
CTAGTGTGTGCCGCTGCCACAGGAACCTTGCTACTGTAATGAGCGAAGCTGACCTCAGTG
CCTCTGGGATCCCGGAGGGCGTAACCGTACTCTACCTCCACAACAAACCAATTATAATGC
TGGATTTCCTGCAGAACACTGACAAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC
AACTGGACGAATTCCCCATGAACACCTCCAAGAATGTCAAGAGTTCTCATTGCAAGGAAAAC
AATATTCAAGACCATTTCACGGGCTGCTCTGCCCAGCTCTGAAAGCTTGAAGAGCTGCACCT
GGATGACAACCTCCATATCCACAGTGGGGTGGAAAGACGGGCTTCCGGAGGCTATTAGCC
TCAAATTGTTGTTTGTCTAAGAACCTGAGCAGTGTGCCTGTTGGCTTCTGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTATCCACATGGCCTTCCAGAA
TCTCACGAGCTGGAGCGTCTTATTGTTGAGCGGAACCTCCTGACCAACAAGGGTATGCCG
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTCATTGTAATTGCTGTCC
CACCCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGCAAGGACAACCAGAT
AAACCACATTCTTGTACAGCCTCTCAAATCTCGCTAACGCTGGAAACGGCTGGATATATCCA
ACAACCAACTCGGGATGCTGACTCAAGGGTTTGATAATCTCTCCAAACCTGAAGCAGCTC
ACTGCTCGGAATAACCCCTGGTTTGACTGCACTTAAATGGGTACAGAATGGCTCAA
ATATATCCCTCATCTCAACGTGCGGGTTCATGTGCCAAGGTCTGAACAAGTCGGG
GGATGCCGTAGGGAAATTAAATATGAATCTTGTCTGTCCCACGACCCCCGGCCTG
CCTCTTCAACCCAGCCCCAAGTACAGCTCTCCGACCACCTCAGCCTCCCACCCCTCTAT
TCCAAACCCTAGCAGAACGCTACACGCCTCCAACCTCTACCACATCGAAACCTCCCACGATT
CTGACTGGGATGGCAGAGAAAGAGTGACCCCACCTATTCTGAACGGATCCAGCTCTATC
CATTGTAATGATACTTCAAGTCAGCTGGCTCTCTCTTCAACCGTGATGGCATA
CAAACTCACATGGGTAAAATGGCCACAGTTAGTAGGGGATCGTTCAGGAGCGCATAG
TCAGCGGTGAGAACACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT
TGTTAGTGCCACTGGATGCTTTAACTACCGCGGGTAGAAGACACCATTGTTAGAGGC
CACCAACCATGCCCTCTATCTGAACAAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
CGTCCCACAGCATGGCTCCCCCTTCTGCTGGCGGGCTTGATGGGGCGCGGTGATATT
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CCAGAAGTGGAAATACAACCGGGCGGGAAAGATGATTATTGCGAGGCAGGCACCAAGA
AGGACAACCTCCATCCTGGAGATGACAGAAACCAGTTTCAGATCGTCTCCTTAAATAACGAT
CAACTCTTAAAGGAGATTCAGACTGCAGCCATTACACCCAAATGGGGCATTAAATTA
CACAGACTGCCATATCCCCAACAAACATGGGATACTGCAACAGCAGCGTGCAGACCTGGAGC
ACTGCCATACGTGACAGGCCAGAGGCCAGCGTTATCAAGGGGACAATTAGACTCTTGAGAA
CACACTCGTGTGTCACATAAAGACACGCAGATTACATTGATAATGTTACACAGATGCAT
TTGTCATTGAATACTCTGTAATTATACGGTGTACTATATAATGGGATTAAAAAGTG
CTATCTTCTATTCAAGTTAATTACAAACAGTTGTAACCTTGCTTTAAATCTT

FIGURE 13

MGLQTTKWPShGAFFLKS~~WLI~~ISLGLYSQVS~~KLL~~ACPSVCRCDRN~~FVY~~CNERSLTSVPLGIP
EGVT~~VLY~~LHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNL~~PKN~~VRVL~~H~~QENNIQTI
SRAALAQLL~~K~~LEELH~~LD~~NS~~I~~STVGVEDGAFREAI~~SL~~KL~~L~~FLSKNHLSSVPVGLPVDLQELR
VDENRIAVISDMAFQNL~~T~~SLERL~~I~~VDGN~~LL~~TNKGIAEGTFS~~H~~TLK~~E~~FSIVRNSLSH~~PP~~D
LPGTHL~~I~~R~~L~~Y~~L~~QDNQINH~~I~~PLTA~~F~~SNLRK~~L~~DISNNQ~~L~~RMLTQGVFDNL~~S~~NLK~~Q~~L~~T~~ARNN
PWFCDCS~~I~~KWVTEWLKY~~I~~PSSLNVRGFM~~C~~QGPEQVRGMAVRELNM~~N~~LLSCPTTPGLPLFTP
APSTASPTTQP~~P~~TLS~~I~~PNPSRSY~~T~~PPT~~T~~SKL~~T~~IPDWDGR~~R~~ERV~~T~~PP~~I~~SERIQLSIHFVND
TSIQVSWL~~S~~LFTVMAYKLTWVKM~~G~~H~~S~~LVGGIVQERIVSGE~~K~~QHLSLVNLEPRSTYR~~I~~CLVPL
D~~A~~FNYRAVEDT~~I~~CSEATTHASYL~~N~~NGSNTASSHEQTTSH~~S~~MGSPF~~L~~LAGL~~I~~GGAVIFV~~V~~V~~L~~
LSVFCW~~H~~M~~H~~K~~K~~GRY~~T~~SQ~~K~~W~~K~~Y~~N~~R~~R~~K~~D~~DY~~C~~EAGTKKD~~N~~SILEM~~T~~TSFQIV~~S~~L~~N~~NDQ~~L~~LKG
DFRLQ~~P~~IY~~T~~PNGGINY~~T~~D~~C~~H~~I~~P~~N~~N~~M~~RY~~C~~N~~S~~SVP~~D~~LEH~~C~~HT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

FIGURE 15

MEKMLAGCFLLILGQIVLLPAEARERSRGRSISRGRHARTHPOQTALLESSCENKRADLVFII
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV
KMRHLSTGTMGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD
TGILIFAIVGQVDFNLTKSIGSEPHEDHVFLVANFSQIETLTSVFKQLCTAHMCSTLEHN
CAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNPGSFVCQCYSGYA
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKGPC
EHECVNMEESYYCRCHRGYTLDPNGKTCRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSRGKTCAKLDSCALGDHGCE
HSCVSSEDSFVCQCPEGYILREDGKTCRKKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLA
EDGKRCRCKDVCKSTHGCEHICVNNNGNSYICKCSEGFLVLAEDGRRCKKCTEGPIDLVFVID
GSKSLGEENFEVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA
HMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEASKAKAN
GITMYAVGVGKAIEEELQEIASEPTNKHLFYAEDFSTMDEISEKLKKGICEALEDSDGRQDS
PAGELPKTVQQPTESEPVTTINIQDLLSCSNFAVQHRYLFEDNLLRSTQKLSHSTKPGSPL
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCGTCGCCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGCGCTGGCGCCCTGACTCCGTCCGGCCAGGGAGGGC
CATGATTTCCCTCCGGGGCCCTGGTGACCAACTTGCTGCCGTTTGTTCCTGGGCTGA
GTGCCCTCGGCCCTCGCGGGCCAGCTGCAACTGCACCTGCCGCAACCGGTTGCAG
GCGGTGGAGGGAGGGAAAGTGGTGCTTCCAGCGTGGTACACCTGACGGGAGGTGTCTC
ATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCCTACATCAATGGGTACAACAAGCAAACCTGGAGTATCCTGGTCTACTCC
ATGCCCTCCCAGAACCTGTCCTCGCGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCTA
CAGCTGCTCCGTGAATGTCAAGACAAACAAGGAAATCTAGGGCCACAGCATAAAACCT
TAGAACTCAATGTAATGGTCCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCAT
GTGGGGCAAACGTGACCTGAGCTGCCAGTCTCCAAGGAGTAAGCCGCTGTCATACCA
GTGGGATCGGCAGCTTCCATCCTCCAGACTTCTTGACCCAGCATTAGATGTCATCCGTG
GGTCTTAAGCCTCACCAACCTTCGTCTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC
AATGAGGTGGGCACTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGCCCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGTGGTACCTGGTGGACTGGGTTGCTGGCTGGCTGGTCC
TCTTGTAACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGGACCTGCCCTGGCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCC
TTCCTCTGTCACCTCCGCACGAGCCCTCCGGCCACCCATGGCCCTCCAGGCCTGGTGCAT
TGACCCCCACGCCAGTCTCCAGCCAGGCCCTGCCCTACCAAGACTGCCACGACAGAT
GGGGCCCACCCCTCAACCAATATCCCCCATCCCTGGTGGGTTCTCCTCTGGCTGAGCCG
CATGGGTGCTGCTGTGATGGTGCCTGCCAGAGTCAGCTGGCTCTGGTAT**TGATGAC**
CCCACCACTCATGGCTAAAGGATTGGGCTCTCCTCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCACCTCTC
TTTACTGTGGAAAACCCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTATGAAGCCAGCTG
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCAGTGAGTCTCCAGGC
CCCCTGATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGT
ATTGATATAACCTGTCAGGCTGGCTGGTAGGTTACTGGGGCAGAGGATAGGAAATCTC
TTATTAAGACTAACATGAAATATGTGTTTTCAATTGCAAATTAAAGATAACATAA
TGTGGTATGAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGHQEKDGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSKPAVQYQ
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTACQCNVTLEVSTGPGAA
VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAAPRTLWPWPKSSDTISKNGTL
SSVTSARALRPHPGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSR
MGAVPVMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCACCACTGCGGCCACCGCCAATGAAACGCCTCCGCTCTAGGGTTTTCCACTTTG
TTGAATTGTTCTATACTCAAAATTGCAAGCACCTGCTCCAAATGCAAATGTGA
AATACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTCAGGAATGGTGTACAA
TTTGTGAAGATGATAATGAATGTGAAATTAACTCAGTCCTGTGGCGAAAATGCTAATTGC
ACTAACACAGAAGGAAGTTATTATTGTATGTGTACCTGGCTCAGATCCAGCAGTAACCA
AGACAGGTTTATCACTAATGATGGAACCCTGTATAGAAAATGTGAATGCAAATGCCATT
TAGATAATGTCTGTATAGCTGAAATATTAATAAAACTTAACAAAAATCAGATCCATAAAA
GAACCTGTGGCTTGTACAAGAAGTCTATAGAAATTCTGTGACAGATCTTCACCAACAGA
TATAATTACATATATAGAAATTAGCTGAATCATCTCATTACTAGGTTACAAGAACAAACA
CTATCTCAGCCAAGGACACCCTTCTAATCCTAACTCAACTCTTACTGAATTGAAAAACCGTGAAT
AATTTGTTCAAAGGGATACTTGTAGTTGGACAAGTTATCTGTGAATCATAGGAGAAC
ACATCTTACAAAATCAGTGCACACTGTTGAAACAGCTACTTAAGGATATCCAGAGCTTCC
AAAAGACCACAGAGTTGATAACAAATTCAACGGATATAGCTCTCAAAGTTTTGAT
TCATATAACATGAAACATATTCTCATATGAATATGGATGGAGACTACATAAATATATT
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATA
AGAGTATTGGCTTTGCTTCATCATCTGACAACCTTATTGAAACCTCAAATTATGAT
AATTCTGAAGAGGGAGGAAAGAGTCATATCTTCAGTAATTTCAGTCTCAATGAGCTCAAACCC
ACCCACATTATATGAACATTGAAAAAAATAACATTACATTAAGTCATGAAAGGTACAGATA
GGTATAGGAGTCTATGTGCATTGGATTACTCACCTGATACCATGAAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT
GACACATTTGCAATTGATGTCCTCTGGCCTTCCATTGGTATTAAAGATTATAATT
TTACAAGGATCACTCAACTAGGAATAATTATTCACTGATTGCTTGCCATATGCATT
ACCTTCTGGTCTTCAGTGAATTCAAAGCACCAGGACAACAATTCAAACAAATTCTTGCTG
TAGCCTATTCTTGCTGAATTGTTCTTGTGGATCAATACAAATACTAATAAGCTCT
TCTGTTCAATCATTGCCGGACTGCTACACTACTTCTTTAGCTGCTTTGATGGATGTGC
ATTGAAGGCATACTCTATCTCATTGTTGTTGTCATCTACAACAAGGGATTTGCA
CAAGAATTTTATATCTTGCTATCTAACGCCAGCGTGGTAGTTGGATTTCGGCAGCAC
TAGGATACAGATATTATGGCACAACCAAGTATGTTGGCTTAGCACCAGAAACAACTTATT
TGGAGTTTATAGGACCAGCATGCCATTCTGTTAATCTCTGGCTTTGGAGTCAT
CATATAACAAAGTTTCGTCAACTGCAGGGTTGAAACCAAGTAGTTGCTTGAGAAC
TAAGGTCTGTGCAAGAGGAGCCCTCGCTCTGTTCTCTCGGCACCACCTGGATCTT
GGGTTCTCATGTTGACGCATCAGTGGTTACAGCTTACACTTCAAGTCAGCAATGC
TTTCCAGGGATGTTCATTTTATTCTGTGTTTATCTAGAAAGATTCAAGAAGAAT
ATTACAGATTGTTCAAAATGCCCCCTGTTGTTGGATGTTAAGGTAAACATAGAGAAATG
GTGGATAATTACAACGTGCACAAAATAAAATTCCAAGCTGTGGATGACCAATGTATAAAA
TGACTCATCAAATTATCCAATTAACTACTAGACAAAAGTATTAAATCAGTTTCT
GTTTATGCTATAGGAACGTGAGATAATAAGGTAATTATGTATCATATAGATATACTATGT
TTTCTATGTGAAATAGTCTGTCAAAATAGTATTGCAAGATATTGGAAAGTAATTGGTT
CTCAGGAGTGTATCACTGCACCCAAAGGAAAGATTTCTTAACACGAGAAGTATGAA
TGTCTGAAGGAAACCACGGCTGATATTCTGTGACTCGTGTGCCTTGAAACTAGTCC
CCTACCACCTCGGTAAATGAGCTCCATTACAGAAAGTGGAACATAAGAGAATGAAGGGCAGA
ATATCAAACAGTGAAGGAAATGATAAGATGTATTGAAATGAACTGTTTCTGTAGAC
TAGCTGAGAAATTGTTGACATAAAATAAAGAATTGAAGAAACACATTACCAATTGAA
TTGTTCTGAACCTAAATGTCCACTAAACAACTTAGACTTCTGTTGCTAAATCTGTTCTT
TTCTAATATTCTAAAAAAAGGTTACCTCCACAAATTGAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 19

MKRLPLVVVFSTLLNCYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIENVANCHLDNCIAA
NINKTLTKIRSIKEPVALLQEYVRNSVTDLSPTDIITYIEILAESSLLGYKNNTISAKDTL
SNSTLTEFVKTVNNFVQRDTFVWDKLSVNRRTHTKLMHTVEQATLRIQSFKQTTEFDT
NSTDIALKVFFFDSYNMKHIHPHMNMDGYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS
SSDNFLLKPQNYDNSEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDRYRSLCAF
WNYS PDTMNGWSSEGCELTYSNETHTSCRNCNLTHFAILMSGPSIGIKDYNILTRITQLG
IIISLICLAI CIFTWFFSEI QSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFC SIIAGL
LHYFFLAAFAWM CIEGIHLYLIVVGVIYNKGFLHKNFYIFGYLSPAVVGFSAALGYRYYGT
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVVLHVVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATTTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATAAGAGTAT
TGGTCCCTTGCTTCATCATCTGACAACCTCTTATTGAAACCTCAAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACTTGAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATAGGTATA
GGAGTCTATGTGGCATTGGAAACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTGCAATTGATGTCCTCTGGTCCTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTCAGTATTGTCTGCCATATGCATTTTACCTTC
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA

FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGGTGGGAGGGAGTTCCCCGAAACCCGGCCG
CTAAGCGAGGCCTCCTCCTCCCGCAGATCCGAACGGCCTGGCGGGGTACCCCGGCTGGGA
CAAGAAGCCGCCCTGCCCTGCCGGGGGGGGGGGGCTGGGCTGGGCGAGGCG
GGTGTGAGTGGGTGTGCGGGGGGGCGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG
TGTCTGGCACCTACCGTGGGCCCCGTAAGGCCTACTATATAAGGCTGCCGGCCGGAG
CCGCCGCGCCGTAGAGCAGGAGCGCTCGTCCAGGATCTAGGGCACGACCATCCAAACCC
GGCACTCACAGCCCCCAGCGCATCCCGTGCAGCCTCCGACCCCATGCCGG
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGGTGGTCCACGTATGG
ATCCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGCGCCCCCTCGCCTCTCGGACGCGGGGCC
CCACGTGCACTACGGCTGGGGCGACCCCATCCGCTGCACCTGTACACCTCCGGCCCC
ACGGGCTCTCAGCTGCTTCTGCATCCGTGCCGACGGCGTGTGGACTGCGCGGGGC
CAGAGCGCAGCAGTTGCTGGAGATCAAGGCAGTCGCTCTCGGGACCGTGGCATCAAGGG
CGTGCACAGCGTGCAGTACCTCTGCATGGCGCCAGGCAAGATGCAGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
TCCGAGAAGCACCGCCTCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA
CAGAGGCTTCTTCCACTCTCTCATTCTCCTGCCATGCTGCCATGGTCCAGAGGAGCCTG
AGGACCTCAGGGGCCACTTGAATCTGACATGTTCTTCGCCCCCTGGAGACCGACAGCATG
GACCCATTGGCTTGTACCCGACTGGAGGCCGTGAGGAGTCCAGCTTGAGAAGTAAC
GAGACCATGCCGGCCTTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGACG
TGCTTCTACAAGAACAGTCCTGAGTCCACGTTCTGTTAGCTTAGGAAGAACATCTAGAA
GTTGTACATATTCAAGAGTTCCATTGGCAGTGCCAGTTCTAGCCAATAGACTTGTCTGAT
CATAACATTGTAAGCCTGTAGCTGCCAGCTGCTGCCCTGGCCCCCATTCTGCTCCCTCGA
GGTTGCTGGACAAGCTGCTGCACTGTCAGTTCTGCTGAATACCTCCATCGATGGGAAC
TCACTTCCTTGGAAAATTCTTATGTCAAGCTGAAATTCTCTAATTCTCATCACTTC
CCCAGGAGCAGCCAGAACAGACAGGCAGTAGTTAATTCAAGAACAGGTGATCCACTGT
AAACAGCAGGTAAATTCACTCAACCCATGTGGAAATTGATCTATCTACTTCCAGGG
ACCATTGCCCTCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGCCACCAAG
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACTTGAGAATTCCCC
CTGAGGCCAGTTCTGTCATGGATGCTGCTGAGAATAACTTGCTGTCCCAGTGTACCTGC
TTCCATCTCCAGCCACCCAGGCCACTGCCACCTCACATGCCCTCCCATGGATTGGGCCT
CCCAGGCCCCCACCCTATGTCAACCTGCACTTCTGTTCAAAAATCAGGAAAAGAAAAGAT
TTGAAGACCCCAAGTCTGTCAATAACTTGCTGTGGAAAGCAGCGGGGAAGACCTAGAAC
CCTTCCCCCAGCACTGGTTCCAACATGATATTATGCCCCAAATTATATTATGTATGTAAGT
TCTCTTATTCTACATTATTATGCCCCAAATTATATTATGTATGTAAGTGGAGGTTG
TTTGTATATTAAAATGGAGTTGTTGT

FIGURE 22

MRSGCVVVHVWILAGLWAVAGRPLAFSDAGPHVHYGWGDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLIEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEE
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

TOEET TOE BEEFTRUCK

CCCAGAACGTTCAAGGGCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCCTGACCTCCTCA
GAGCAGCCGGCTGCCGCCGGGAAGATGGCGAGGAGGAGCCGCCACGCCCTCCTGCTG
CTGCTGCGCTACCTGGTGGCTGCCCTGGGCTATCATAAGGCCTATGGGTTTCTGCCCAAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGCAAAACCCAA
AGAAGACTGTTCCAGATTAGAGTGGAAAGAAACTGGGTCGGAGTGTCTCCTTGTCTAC
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG
GATCAAAATGTGACAAGAAGTGATGCGGGAAATATCGTTGTGAAGTTAGTGCCTCATCTG
AGCAAGGCCAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCCTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGAAATCCAGCTCCTGAATAACACATGGTTAAGGATGGCATCGTTGCTAGAAA
ATCCCAGACTGGCTCCAAAGCACCAACAGCTCATACACAATGAATAACAAAAACTGGAAC
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAATATTCTGTGAAGCCCGCAATT
TGTTGGATATCGCAGGTGTCCTGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTAGTGATTTCCGTTGTGGCCTTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTCAAAAGAAACCTCCTCCAGAAGAGTAATTCTCATCTAA
AGCCACGACAATGAGTAAAATGTGCAGTGGCTACGCCCTGTAATCCCAGCACTTGGAAAGG
CCGGCGGGCGGATCACGAGGTCAGGAGTTCTAGACCAGTCTGGCAATATGGTGAACCC
CATCTCTACTAAAATACAAAATTAGCTGGCATGGTGGCATGTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAATCACTGAACCCGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTAAAAAATAAAATAAAATA
AATAAAATACTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATT

FIGURE 24

MARRSRHRLLLLLLRLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLE
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQNLLED
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKD GIRLLENPRLGSQST
NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNI SGIIIAAVVVA
LVISVCGLGV CYAQRKGYFSKETSFQKSNSSSKATTMSENVWLTPVIPALWKA AAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGGCAACATTATTAACATGCTCCACAGCCGGACCTGGCAT
CATGCTGCTATTCTGAAATACTGAAGAAGCATGGGATTAAATATTTACTTCTAAATAA
ATGAATTACTCAATCTCCTATGACCATCTACATACTCCACCTTCAAAAGTACATCAATA
TTATATCATTAAGGAAATAGTAACCTCTCTCCAAATATGCATGACATTTGGACAATG
CAATTGTGGCACTGGCACTTATTCAGTGAAGAAAAACTTGTGGTTCTATGGCATTCA
TTTGACAAATGCAAGCATTCTCCTATCAATCAGCTCTATTGAACCTACTGACTG
TGGAATCCTTAAGGGCCATTACATTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT
CCGAATTCTATGTGCTACTTGGCTAGCTACTACACTAGTACAAGCTGTAGATAAAAAAG
TGGATTGTCCACGGTTATGTACGTGTAAATCAGGCTTGGTTACACCCAGATCCATTAT
ATGGAAGCATTACAGTGGATTGTAAATGATTAGGTCTTTAACTTCCCAGCCAGATTGCC
AGCTAACACACAGATTCTCTACAGACTAACAAATATTGCAAAATTGAATACTCCACAG
ACTTCCAGTAAACCTACTTGGCTGGATTATCTCAAAACAAATTATCTCAGTCACCAAT
ATTAATGTAAAAAGATGCCTCAGCTCTTCTGTGTACCTAGAGGAAAACAAACTTACTGA
ACTGCTGAAAAATGTCGAGCAACTTACAAGAACTCTATATTAAATCACAAC
TGCTTCTACAATTTCACCTGGAGCCTTATTGGCCTACATAATCTTCTTCGACTTCATCTC
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTGATGCTCTCCAAATCTAGAGAT
TCTGATGATTGGGGAAAATCCAATTATCAGAATCAAAGACATGAACCTTAAGCCTCTTATCA
ATCTCGCAGCTGGTTAGCTGGTATAAACCTCACAGAAATACCAAGATAACGCCTGGTT
GGACTGGAAAACCTAGAAAAGCATCTCTTACGATAACAGGCTTAAAGTACCCATGT
TGCTCTCAAAAAGTTGTAAATCTCAAATTGGATCTAAATAAAATCTTAAATAGAA
TACGAAGGGGTGATTAGCAATATGCTACACTTAAAGAGTTGGGATAAAATAATGCT
GAGCTGATTCCATCGATAGTCTGCTGGATAACCTGCCAGATTAAAGAAAATAGAAGC
TACTAACAAACCTAGATTGTCTTACATTCAACCCATGCATTTCAGACTCCCCAAGCTGG
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCTGAGTC
CCAAACCTCAAGGAAATCAGCATAACACAGTAACCCATCAGGTGTACTGTGTCATCCGTTG
GATGAACATGAACAAACCAACATTGATTGATGGCCAGATTCACTGTTGCGTGGACC
CACCTGAATTCCAAGGTAGAATGTCGGCAAGTCGATTCAAGGGACATGATGGAAATTGT
CTCCCTCTTAACTGCTCTGAGAGCTTCTTAATCTAAATGTAAGCTGGAGCTATGT
TTCCCTTCACTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTTCTG
GTCAAAAACCTTGCCTAATACCCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAAACACTA
GATAAAATGGCGTAACCTCCAAAGAAGGGGTTATATACTGTATAGCAACTAACCTAGT
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTCCACAAGATAACAAATG
GCTCTTGAATATTAAAATAAGAGATATTCAAGGCCAATTCACTGTTGGTGTCTGGAAAGCA
AGTTCTAAAATTCTCAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAATTCTCA
TGCTGCGCAAAGTGTGAATACCATCTGATGTCAGGTATATAATCTTACTCATCTGAATC
CATCAACTGAGTATAAAATTGTATTGATATTCCACCATCTATCAGAAAACAGAAAAAA
TGTGTAAATGTCACCACCAAGGTTGCACCCCTGATCAAAAGAGTATGAAAAGAATAATAC
CACAAACACTTATGGCCTGTCTGGAGGCCTTCTGGGATTATTGGTGTGATATGTCTTATCA
GCTGCCCTCTCCAGAAATGAACGTGTGATGGTGACACAGCTATGTGAGGAATTACTACAG
AAACCAACCTTGCATTAGGTGAGCTTATCCTCTGATAAAATCTCTGGGAAGCAGGAAA
AGAAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTATAGGTTACCAACAAATATGTCCT
AAAAACCAAGGAAACCTACTCCAAAATGAAC

FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKVDCPRLCTCEIRPWFTPRSIVMEASTVDCNDLGLLT
FPARLPANTQILLQTNNAKIEYSTDFTPVNLTGQLDSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTELPEKCLSELSNLQELYINHNLSTISPGAFIGLHNLLRLHLSNRLQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPLINLRLSLVIAGINLTEIPDNALVGLENLESISFYDNRL
IKVPHVALQKVNLKFIDLNKNPINRIRRGDFSNMLHLKELGINNMPELISIDSALVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSALYHGTIESLPNLKEISIHSNPIRC
DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGQNVQVHFRDMMEICLPLIAPESFPSNLNV
EAGSYVSFHCRATAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLINGVTPKEGGLYTC
IATNLVGADLKSVMIKVDGSPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFV
KTENSHAAQSARI PSDVKVYNLTHLN PSTEYKICIDIPTIYQKNRKKCVN VTTKGLHPDQKE
YEKNNTTTLMACLGGLLGIIGVICLISCLSPEMNC DGGHSYVRNYLQKPTFALGELYPPLIN
LWEAGKEKSTSLKVKATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

GCCTGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTAC
CACGCTTGTGGAGTAGATGAGGAATGGGCTCGTGAATTATGCTGACATTCCAGCATGAATCT
GGTAGACCTGTGGTTAACCGTTCCCTCCATGTGTCTCCTCCTACAAAGTTTGTCTTA
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCAAGGGCTGTCTTGTCTCCTCTGGG
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTCCTCCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTTAAGG
ACCTCCATCAACTGAGAGTTCTAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCAT
GCCTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAATGCCCTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC
AACGTGATCTGTAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTGTAAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTTGGCTGGTCACTATGGTATCTCATATGTGGTATATTATGTGAGGCAAATCAGGAG
GATGCCCGGAGACACCTCGAATACTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAAACTGACTGTCATTGAGAAAGAAAGAAA
GTAGTTGCGATTGCAGTAGAAATAAGTGGTTACTTCTCCCATCCATTGTAAACATTGAA
ACTTGTATTCAGTTTTTGAAATTATGCCACTGCTGAACTTAAACAAACACTACAACA
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAAATAATGAAATTATTTTT
AATTAAAAGCAAATAAAAGCTTAACCTTGAACCATTGGGAAAAAAAAAAAAAAACA

FIGURE 28

MNLVDLWLTRSLSMCLLQSfvLMILCFHSASMC PKGCLSSSGLNVTCSNANLKEIPRDL
PPETVLLYLDSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDLSDNR
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPF
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGGCCGAGATGCAGGTGAGCAAGAGGATGCTGGGGGGGG
GGCGTAGGGAGCATGCCAGCCCCCTCTGGCCTGCTGGCAGCCCACCTCTCTGCTGGTGCT
GGGCTCAGTGTCTAGGCTCGGCCACGGCTGCCGCCCCGCTGCGAGTGCTCCGCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTGTGGCAGTCCCCGAGGGCATCCCCACCGAG
ACGCGCCTGCTGGACCTAGGCAAGAACCGCATAAAAGCTCAACCAGGACGAGTTGCCAG
CTTCCCGCACCTGGAGGAGCTGGAGCTAACGAGAACATCGTGAGCGCCGTGGAGGCCGCG
CCTTCAACAAACCTCTAACCTCCGGACGCTGGGCTCCGAGCAACCGCCTGAAGCTCATC
CCGCTAGGCGTCTTCAGCAACCTGACCAAGCAGGACATCAGCAGAGAACAAAGAT
CGTTATCCTACTGGACTACATGTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCACCGGCCCTCAGCGGCCCTAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGGCTGTCCCACCTGCACGCC
CATCGCTCTGAGGCTCCGGCACCTAACATCAATGCCATCCGGACTACTCCTTAAGAGGC
TGTACCGACTCAAGGTCTGGAGATCTCCACTGGCCTACTGGACACCATGACACCCAAC
TGCCTCTACGGCTAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCGTCCGCCACCTAGTCTATCTCGCTTCTAACCTCTCCTAACACCCATCA
GCACCAATTGAGGGCTCCATGTTGATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGC
GGCAGCTGGCGTGGTGGAGGCCCTATGCCTTCCGGCCCTAACACTACCTGCGCGTGTCAA
TGTCTCTGGAACCAAGCTGACCAACTGGAGGAATCAGTCTTCACTCGTGGCAACCTGG
AGACACTCATCTGGACTCCAACCGCTGGCCTGCGACTGTCGGCTCTGTGGGTGTTCCGG
CGCCGCTGGCGCTCAACTCAACCGGAGCAGGCCACGTGCGCCACGCCAGGTTGTCCA
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCAACTACTTCACCTGCCCGCG
CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTGTGGACGAGGGCACACGGTGCAGTT
GTGTGCCGGGCGATGGCGACCCGCCGCCATCCTCTGGCTCTACCCGAAAGCACCT
GGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTCCCTGATGGCACGCTGGAGGTGCGCT
ACGCCAGGTACAGGACAAACGGCACGTACCTGTGATGCCAACCGGGCGAACAGAC
TCCATGCCGCCACCTGCATGTGCGCAGCTACTGCCGACTGGCCCCATGACCAACAA
GACCTCGCTTCATCTCCAACCAGCCGGGAGGGAGAGGCCAACAGCACCCGCCACTG
TGCCTTCCCCCTGACATCAAGACCTCATCGCCACCACTGGCTCATCTCTTC
CTGGCGTGTCTCTTCTGCCCTGGTGTGCTGTTCTGGAGGCCGGCAAGGGCAACAC
AAAGCACAAACATCGAGATCGAGTATGTGCCCGAAAGTCGAGCAGGATCAGCTCCCG
ACGCGCCCCGCAAGTTCAACATGAAGATGATATGAGGCCGGGCGGGGGCAGGGACCCCG
GGCGGGCGGGCAGGGGAAGGGCCTGGTGCACCTGCTACTCTCAGTCCCTGCCACCTC
CTCCCTACCCCTCTACACACGTTCTTCTCCCTCCGCTCCGCTCCCTGCTGCCCG
CCAGCCCTCACCACTGCCCTCTTCTACAGGACCTCAGAACGCCAGACCTGGGACCCCA
CCTACACAGGGCATTGACAGACTGGAGTTGAAAGCCGACCGACACGCCAGAGTCA
ATAATTCAATAAAAAAGTTACGAACCTTCTCTGTAACCTGGGTTCAATAATTATGGATT
TATGAAAACCTGAAATAATAAAAAGAGAAAAAAACTAAAAAAACAAAAAA

FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELENENIVSAVEPGAFNNLFNLRTL
GLRSNRLKLIPLGVFTGLSNLTKQDISENKIVILLDYMFDQLYNLKSLEVGDNDLVYISHRA
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVLEISH
WPYLDLTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMHLHEL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVNVSGNQLTTLEESVFHSGVNLETLILDSNPLA
CDCRLLWVFRRRWRLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPIALWLSPRKHLVSAKSNGRLTVFPDGTLEVRYAQVQDNGTYL
CIAANAGGNDNSMPAHLHVRSYSPDWPQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCVLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCCACCGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTCGGTCAAC
ATCGTAGTCCACCCCTCCCCATCCCCAGCCCCGGGATTCAAGGCTCGCCAGCGCCAGCC
AGGGAGCCGGCCGGGAAGCGCG**A**TGGGGCCCCAGCCGCTCGCTCCTGCTCCTGCTCCTGC
TGTTCGCCTGCTGCTGGCGCCGGCGGGCCAACCTCTCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGCACCCTGGTGGCTCAAGTGCCAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGCTAACCCCTGCTCAGCAGACTCTACTTGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTCACTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCGT
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAACCCATCATCACTGGTT
ATAAAATCTTCATTACGGGAAAAGACACAGCCACCCCTAAACTGTCAGTCTTCTGGGAGCAAG
CCTGCAGCCGGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCGCAT
ACAGGAAGATCCAATGGTAAAACCTTCACTGTCAGCAGCTGGTACATTCCAGGTTACCC
GGGAGGATGATGGGGCGAGCATTGAGTAAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTCCCTTCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCA
CAACATGGGCAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTGCCT
CCTCCTCCAGCACCTACCACGCCATCATCGGTGGATCGTGGCTTCATTGTCTCCTGCTG
CTCATCATGCTCATCTCCTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGAAAAGGCTCCGACGATGCTCCAGACGGACACGGCCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTCT**A**GGGCGCTGCCACTTCCTGC
GCCCCAGGGCCCTGTGGGACTGCTGGGCCGTACCAACCCGGACTTGTACAGAGCAA
CCGCAGGGCCGCCCTCCGCTTGCTCCCCAGCCCACCCACCCCTGTACAGAAATGTCTGC
TTTGGGTGGTTTGACTCGGTTGGAATGGGAGGGAGGAGGGCGGGGGAGGGAGGG
TTGCCCTCAGCCCTTCCGTGGCTCTGCATTGGTTATTATTATTTGTAACAATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGTGAGAAAAGCAAAAACA
AACAAAAAACAA

FIGURE 32

MGAPAASLLLLLFAACCWAPGGANLSQDDSQWPWTSDETVVAGGTVVLKCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRQLVTSTPHELSIISNVALADEGEYTCISIFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKS DSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTTCTCCTTCTGG
CTTCGGACATTGGAGCACTAAATGAACCTGAATTGTGTCGTGGCGAGCAGGATGGTCGCTG
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTAAAAATGCTGCTTGGATTCTGTT
GCTGGAGACGTCTTTGCGCTGGAAACGTTACAGGGACGTTGCAAAGAGAAGA
TCTGTCCTGCAATGAGATAGAAGGGACCTACACGTAGACTGTGAAAAAAAGGGCTTCACA
AGTCTGCAGCGTTCACTGCCCGACTTCCAGTTACCATTTATTCATGGCAATT
CCTCACTCGACTTTCCCTAATGAGTTGCTAACCTTATAATGCGGTTAGTTGCACATGG
AAAACAATGGCTTGCATGAAATCGTCCGGGGCTTTCTGGGGCTGAGCTGGTAAAAGG
CTGCACATCAACAACAAGATCAAGTCTTTCGAAAGCAGACTTTCTGGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTTAATTATTACGAGATATAGACCCGGGGCTTCCAGG
ACTTGAACAAAGCTGGAGGTGCTCATTTAAATGACAATCTCATCAGCACCCACCTGCCAAC
GTGTTCCAGTATGTGCCATCACCCACCTCGACCTCCGGGTAACAGGCTGAAAACGCTGCC
CTATGAGGAGGTCTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCC
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC
CTGATCGGCCGAGTGGTCTGCGAAGCCCCACAGACTGCAGGGTAAAGACCTCAATGAAAC
CACCGAACAGGACTTGTGTCCTTGAAAAAACGAGTGGATTCTAGTCTCCCGCGCCCC
CCCAAGAACAGGACCTTGCTCCTGGACCCCTGCCAACCTCCCTTCAAGACAAATGGCAAGAG
GATCATGCCACACCAGGGTCTGCTCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT
CAAATCAGACCCACAGCAGCGATAGCGACGGTAGCTCCAGGAACAAACCTTAGCTAAC
GTTTACCTGCCCTGGGGCTGCAGCTGCGACCATCCCAGGGTGGTTAAAGATGAAC
TGCAACAACAGGAACGTGAGCAGCTGGCTGATTGAAGCCAAGCTCTAACGTGCAGGA
GCTTTCCCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTTGTGGATTACAAGA
ACCTCATTCTGTTGGATCTGGCAACAATAACATCGCTACTGTAGAGAACAAACACTTCAAG
AACCTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACCGTGTCCGG
GAAATTCGCGGGCTGCAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA
TCCTCCGGGACTTTCAATGCCATGCCAAACTGAGGATCCTCATTCTCAACAAACACTG
CTGAGGTCCCTGCCTGGACGTGTTGCTGGGGCTCGCTCTCTAAACTCAGCCTGCACAA
CAATTACTCATGTACCTCCGGTGGCAGGGGTGCTGGACCAGTTAACCTCCATCATCCAGA
TAGACCTCACGGAAACCCCTGGGAGTGCTCCTGCACAAATTGTGCCCTTCAAGCAGTGGCA
GAACGCTTGGGTCCTGAAGTGCTGATGAGCAGCTCAAGTGTGAGACGCCGGTGAACCTT
TAGAAAGGATTCATGCTCCTCTCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCACGTTAACTTCGACAGTAAAACAGCACTGGTGGCGAGACCGGGACGCACTCC
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTCGTGTGGTCCGGACTGCTGCTGGT
GTTTGTACCTCCGCCTCACCGTGGGGCATGCTCGTGTATTACCTGAGGAACCGAAAGC
GGTCCAAGAGACGAGATGCCAACTCCTCCGCGTCCGAGATTAATTCCCTACAGACAGTCTG
GACTCTCCTACTGGACAATGGGCTTACAACCGAGATGGGCCACAGAGTGTATGACTG
TGGCTCTACTCGCTCTCAGACTAAGACCCCAACCCCAATAGGGGAGGGCAGAGGGAAAGGCG
ATACATCCTCCCCACCGCAGGCACCCGGGGCTGGAGGGCGTGTACCAAATCCCCGCG
CCATCAGCCTGGATGGGCATAAGTAGATAAAACTGTGAGCTCGCACAACCGAAAGGGCCT
GACCCCTACTTAGCTCCCTCCTGAAACAAAGAGCAGACTGTGGAGAGCTGGAGAGCGCA
GCCAGCTCGCTTTGCTGAGAGCCCCTTGACAGAAAGCCCAGCACGACCCCTGCTGGAAG
AACTGACAGTGCCTCGCCCTGGCCCCGGGGCTGTGGGGTTGGATGCCGGTTCTATAC
ATATATACATATCCACATCTATATAGAGAGATAGATACTATTCTTCCCTGTGGATTAG
CCCCGTGATGGCTCCCTGTTGGCTACGCAGGGATGGCAGTTGCACGAAGGCATGAATGTAT
TGTAAATAAGTAACCTTGACTTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTCVCKEKCSCNEIEGDLHVDCCEKKGFTSLQRFTAPTSQFYH
LFLHGNSLTRLFPNEFANFYAVSLHMENGLHEIVPGAFGLQLVKRLHINNNKIKSFRKQ
TFLGLDDLEYLQADFNLLRIDPGAFQDNLKLEVILLNDNLISTLPANVFQYVPITHDLRG
NRLKTLPYEEVLEQIPIGIAEILLEDPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ
GKDLNETTEQDLCPLKNRVDSSLAPPAPPAQEETFAPGPLPTPFKTNGQEDHATPGSAPNGGT
IPGNWQIKIRPTAAIATGSSRNKPLANSLPCPGCSCDHIPGSGLKMNCNNRNVSSLADLKP
KLSNVQELFLRDNKIHSIRKSHFVDYKMLILLLDLGNNNIATVENNTFKNLLDLRWLYMDSNY
LDTLSREKFAGLQNLEYLNVEYNIAIQLILPGTFNAMPKLRILILNNNNLLRSILPVDVFAGVSL
SKLSLHNNYFMYLPVAGVLDQLTSIIQIDLHGNPWECSCTIVPFKQWAERLGSEVLMSDLKC
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL
VPGLLLTVFTSAFTVVGMLVFLRNRKRSKRRDANSASEINSLQTVCDSSYWHNGPYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCCGTACCCGGCCAGCTGTGTCCTGACCCCAGAATAACTCAGGGC
TGCACCGGGCCTGGCAGCGCTCCGACACATTCCTGTCGCGGCCTAAGGGAAACTGTTGGC
CGCTGGGCCCGGGGGATTCTTGGCAGTTGGGGTCCGTCGGAGCGAGGGCGGAGGGG
AAGGGAGGGGAACCGGGTTGGGAAGCCAGCTGTAGAGGGCGGTACCGCGCTCCAGACAC
AGCTCTGCGTCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCAGGGCCTCAG
AGAATGAGGCCGGCGTTCGCCCTGTGCCCTCTGGCAGGGCCTCTGGCCCGGCCGGCG
CGCGAACACCCCAGTCCGACCGTGTGGCTCGGCCCTCGGGGCGCTGCTACAGCTGC
ACCACGCTACCATGAAGCGGCAGGCAGGCCAGGAGGAGGCCTGCATCCTGCGAGGTGGGCGCTC
AGCACCGTGCCTGCCGAGCTGCGCGCTGTGCTCGCCTCTGCGGCCAGGCCAGG
GCCCGGAGGGGCTCAAAGACCTGCTGTTCTGGGTCGCACTGGAGCGCAGGCCTCCCAGT
GCACCCCTGGAGAACGAGCCTTGCAGGGGTTCTCCTGGCTGTCCGACCCGGCGTCTC
GAAAGCGACACGCTGAGTGGGAGGAGGCCAACGCTCCTGCACCGCGGGAGATGCGC
GGTACTCCAGGCCACCGGTGGGTCGAGGCCGAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCCAACGGCTACCTGTGCAAGTACCAAGTTGAGGTCTTGTGCTCTGCGCCGCCGG
GCCGCCCTCTAAGTGGCTATCGCGGCCCTTCAGCTGCACAGGCCGCTCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGACAGCTCCGATCTCAGTTACTGCA
TCGCGGACGAAATCGGCCTCGCTGGACAAACTCTCGGGCGATGTGTTGTCCTGCC
GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAACTGCCTAGACGACTTGGGAGG
CTTGCCCTGCAATGTGCTACGGGCTTCGAGCTGGGAAGGACGGCGCTCTGTGACCA
GTGGGAAGGACAGCCGACCCCTGGGGACCGGGTGCCCACCAGGCGCCGGCCACT
GCAACCAGCCCCGTGCCAGAGAACATGGCAATCAGGGTCGAGGAGAAGCTGGGAGAGAC
ACCACTGTCCCTGAACAAGACAATTCACTAACATCTATTCCCTGAGATTCCCTGATGGGAT
CACAGAGCACGATGTCTACCCCTCAAATGTCCCTCAAGCCGAGTCAAAGGCCACTATCACC
CCATCAGGGAGCGTGAATTCCAAGTTAATTCTACGACTCCCTGCCACTCCTCAGGCTT
CGACTCCTCCTCTGCCGTGGTCTTCATATTGTGAGCACAGCAGTAGTAGTGTGGTGT
TGACCATGACAGTACTGGGCTTGTCAAGCTCTGCTTCACGAAAGCCCCTTCCAGCCA
AGGAAGGAGTCTATGGGCCGCCGGCTGGAGAGTGATCCTGAGCCGCTGCTTGGGCTC
CAGTCTGCACATTGACAAACAATGGGTGAAAGTCGGGACTGTGATCTGCGGGACAGAG
CAGAGGGTGCCTTGGCGAGTCCCTCTTGCTACTGATGCA **AGGAAACAGGG**
CATGGGCACTCCTGTGAACAGTTTCACTTTGATGAAACAGGGAAACCAAGAGGAACCTAC
TTGTGTAAGTACAATTCTGCAGAAATCCCCCTCCTCTAAATTCCCTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCCTCCCTGATGATAGAGGAAGTGGAAAGTGCCTTAGGA
TGGTGTAACTGGGGACGGGTAGTGCCTGGGAGAGATTTCTATGTTATTGGAGAA
TTTGGAGAAGTGAATTCAAGACATTGGAAACAAATAGAACACAATATAATTACAA
TTAAAAAATAATTCTACAAATGGAAAGGAAATGTTCTATGTTGTCAGGCTAGGAGTAT
ATTGGTTGAAATCCCAGGGAAAAAATAAAAAATTAAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEACILRGGALS
TVRAGAELRAVLALLRAGPGPGGGSKDLLFWVALERRSHCTLENEPLRGFSWLSSDPGGLE
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCPAPRPGA
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVVFIFVSTAVVVLVILMTVLGLVKLCFHESPSSQPR
KESMGPPGLESDPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGGCGTGGGATTCAAGCAGTGGCTGTGGCTGCCAGAGCAGCTCCTCAGGGAAACTAAG
CGTCGAGTCAGACGGCACCATATAATCGCCTTAAAAGTGCCTCCGCCCTGCCGCCGCGTATC
CCCCGGCTACCTGGGCCCGCCCGGGCGGTGCGCGCGTGAAGAGGGAGCGCGGGCAGCCGA
GCGCCGGTGTGAGCCAGCGCTGCCAGTGTGAGCGGGCGGTGTGAGCGCGTGGGTGCGGA
GGGGCGTGTGCGCGCGCGCGTGGGGTGCACAAACCCGAGCGTCTACGCTGCCATGA
GGGGCGCGAACGCCTGGCGCCACTCTGCCTGCTGGCTGCCGCCACCCAGCTCTCGCG
CAGCAGTCCCCAGAGAGACCTGTTTACATGTGGTGGCATTCTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTTCTGGAGTGTACCCCTCCAAATAGCAAATGTACTTGGAAAATCA
CAGTCCCAGAGAAAAGTAGTCGTTCTCAATTCCGATTCAAGACCTCGAGAGTGACAAC
CTGTGCCGCTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGCCAGCGCATTGCCG
CTTCTGTGGCACTTCCGGCTGGAGCCCTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
TGATTCTGATGCCAACACAGCTGGCAATGGCTCATGGCCATGTTCTCCGCTGCTGAACCA
AACGAAAGAGGGATCAGTATTGTGGAGGACTCCTGACAGACCTCCGGCTTTAAAAC
CCCCAACTGGCCAGACCGGGATTACCCCTGCAGGAGTCACCTGTGTGGCACATTGTAGCCC
CAAAGAATCAGCTTATAGAATTAAAGTTGAGAAGTGTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTAATGGCGGGGAAGTCAACGATGCTAGAAGAATTGGAAA
GTATTGTGGTGTAGTCCACCTGCACAAATTGTCTGAGAGAAATGAACCTTTATTCACT
TTTATCAGACTTAAGTTAACTGCAGATGGTTATTGGTCACTACATATTCAAGGCCAAA
AAACTGCCTACAACACAGCCTGTCACCACACATTCCCTGTAACCACGGGTTAAA
ACCCACCGTGGCCTGTGTCACAAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTTGTATTAGCCGGCACTGTTATCACAAACCATCACTCGCGATGGGAGTTG
CACGCCACAGTCTGATCATCAACATCTACAAAGAGGGAAATTGGCGATTCAAGGCCGGG
CAAGAACATGAGTGCCAGGCTGACTGTCGTGCAAGCAGTGCCTCTCCTCAGAAGAGGTC
TAAATTACATTATTATGGCCAAGTAGGTGAAGATGGCGAGGCAAAATCATGCCAACAGC
TTTATCATGATGTTCAAGACCAAGAATCAGAAGCTCTGGATGCCTAAAAAATAAGCAATG
TTAACACTGAACGTGTCCATTAAAGCTGTATTCTGCCATTGCCCTTGAAAGATCTATGTT
TCTCAGTAGAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATCCGAAAGATGG
GAAGTGGTTGACTCTTCACATGATGGAGGTATGAGGCCCTCGAGATAGCTGAGGGAAAGTTCTT
TGCCCTGCTGTCAGAGGAGCAGCTATCTGATTGGAAACCTGCCACTTAGTGCCTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTTGGAAAGCGTTATTATACATCTGTAAAAGGAT
ATTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAAGATTTAGAAGTGCAATATTTATAGT
GTTATTTGTTCACCTCAAGCCTTGCCCTGAGGTGTTACAATCTGTCTGCCTTCTA
AATCAATGCTTAATAAAATATTTAAAGGAAAAAA

FIGURE 38

MRGANAWAPLCLLLAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVVLNFRFIDLESNDNLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPPAPIVSERNELLI
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRRTGTLEGN
YCSSDFVLAGTVITTIITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR
GLNYIIMQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGCGGACGCGTGGCGGCCACGGCGCCCGGGCTGGGCGGTGCTTCTT
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGTAAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTTCACACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCGCCTCAGCCCCATCCGTGTCATACTG
CCGGGGACTGGTTGACAGCTTAACAAGGGCTGGAGAGAACCATCCGGACAACTTGGAG
GTGGAAACACTGCCTGGGAGGAAGAGAATTGTCAAATACAAAGACAGTGAGACCCGCCTG
GTAGAGGTGCTGGAGGGTGTGAGCAAGTCAGACTCGAGTGCCACCGCCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTCAAGCAGCAGGAGGCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCCTGC
CTTCCCTGTCTGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGTACGGGGTGAGGCCTGTGGCC
AGTGTGGCCTGGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTGGCTTGT
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGGTCAATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCA
GTGGAGCTGACCAATTCTCGTGAACACTGAGGGCTCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGCAGGGCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTCCGGGAGAGA
ACAAGCAGTGTAAAACACCGAGGGCGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGCAGCAGATGTTCTTGGCATCATCATCTGTGCACTGCCA
CGCTGGCTGCTAAGGGCAGTGGTGTACCGCCATCTCATTGGGCTGTGGCGGCCATG
ACTGGCTACTGGTGTCAAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGAT
ATCGCGGCCACCACTGTAGGACCTCCCTCCACCCACGCTGCCCGAGAGCTTGGCTGCC
TCCTGCTGGACACTCAGGACAGCTTGGTTATTTTGAGAGTGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTCTCACCTGGGGACTGGCAGGCTCACAAATGTGTGA
ATTTCAAAAGTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGGTGGGCCATCACAGCTCCCTGCTGCCAGCTGCATGCTGCCAGTCCCTGT
TCTGTGTTACCAACATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAAGA
AAGGTCTGGAAAGTTAAAAAAAAAAAAAAAAAAAAAA

FIGURE 40

MAPWPPKGLVPAVLWGLSLFLNLPGPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAEEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLESELVESWWFHKQ
QEAPDLFQWLCSDSLKLCGPAGTFGPGCLPCPGGTERPCGGYGCCEGEGTRGGSGHCDCQAG
YGGEACGQCGGLGYFEAERNASHLVCACFGPCARCSGPEESNCLQCKKGWALHHLKVDIDE
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCPGYQQVGSKCLDVDECE
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG
IIICALATLAKGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCCCTCCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCTCTGCTCCTCCAGGGCA
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGCACTCTGGGTGTTGCCCTGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGGCACTGCCAGCTGCTGCCAGCTCAAAGAGGT
GCCCACCCCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGCGAAAGAGGTTAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTGGCGTTGGAGGCCAGCACACACACTGCTGGTGGTCGG
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTCAGGCCGTGCTGCCGCTTCCAGG
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGCGGCTGTCCCCGCGCAGGCCCGGGCC
CGGGTGACCGTCGAGTGGCTGCCGTCCGACGACGGCTCCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG
GAGCATCTGGCCCGCTGGCGTCCGGCCACAAGCTGGTCCGCTTGCCCTCGCAGGGGGC
GCCAGCCGGCTTGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTTGGGACTATGGAG
CTCAGGGCGACTGTGACCCCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGATGAAGTGGGCCAGAACCTGGGCTGGAGCCCCCGGGCTT
CCTGGCTTATGAGTGTGTGGCACCTGCCGGCAGCCCCCGAGGCCCTGGCCTTAAGTGGC
CGTTCTGGGCCTCGACAGTCATGCCCTCGAGACTGACTCGCTGCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCTGCCAGGAGGCTCCAGCCATAGGCGCCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGTGCTGAGGGTACCAAGGAGAGCTG
GCGATGACTGAAGTGCATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT
CCTCTGACAAGTTACCTCACCTAATTGGCTCTCAGGAATGAGAACATTGGCCACTGGA
GAGCCCTGCTCAGTTCTATTCTATTACTGCACATATTCTAACGACTTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCANTGTGTCATTGTTACTTGTCTGTCAC
TGGATCTGGCTAAAGTCCTCACCACCACTCTGGACCTAACGACCTGGGTTAAGTGTGGGT
TGTGCATCCCCAATCCAGATAATAAGACTTGTAAAACATGAATAAACACATTATTCT
AAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSHESGWKAFDVTEAVNF
WQQLSRPRQPLLLQVSQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCCRQPEALAFKWPF
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCCAGGAGTCCTCGGCGGCTGTTGIGTCAGTGGCCTGATCGCGAGGGGACAAA
GGCGCAAGTCGAGAGGAAACTGTTGTGCCTCTCATATTGGCGATCCTGTTGTGCTCCCTGG
CATTGGGCAGTGTACAGTGCACTCTCTGAACCTGAAGTCAGAATTCCCTGAGAATAATCCT
GTGAAGTTGTCCGTGCCTACTCGGGCTTTCTTCTCCCCGTGTGGAGTGGAAAGTTGACCA
AGGAGACACCAACCAGACTCGTTGCTATAATAACAAGATCACAGCTCCTATGAGGACCGGG
TGACCTTCTGCCA**A**CTGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGAACAGCTATGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCTGCCACCATTGGGAACCGGG
CAGTGCTGACATGCTCAGAACAGATGGTCCCCACCTTCTGAATAACACCTGGTTCAAAGAT
GGGATAGTGATGCCTACGAATCCAAAAGCACCCGTGCCTTCAGCAACTCTCCTATGTCC
GAATCCCACAAACAGGAGAGCTGGTCTTGATCCCCTGTCAGCCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTCAAATGCTGTGCGATGGAAAGCT
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCCGTCTTGTAACCTGATTCTCTGGGAAT
CTTGGTTTTGGCATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCTGGTGTGGCCTGGTCGGCTACCGCCTATCATCTGCATTGCCTTACT
CAGGTGCTACCGGACTCTGGCCCTGATGTCTGTAGTTCACAGGATGCCTTATTGTCTTC
TACACCCCACAGGGCCCCCTACTTCTCGGATGTGTTTAATAATGTCAGCTATGTGCC
ATCCTCCTTCATGCCCTCCCTCCCTTACCACTGCTGAGTGGCCTGGAATTGTTAAA
GTGTTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGAAAAATGGCGGGGTGCGAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATCTTGAATAGGTATCTTGAGCTTGGTCTGGCTCTTCTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGGAAATTAGAGGCTAGAGCGGCTGAAAGGTTGGTGG
TGATGACACTGGGGCCTTCCATCTCTGGGGCCACTCTCTGTCTTCCATGGGAAGTG
CCACTGGATCCCTCTGCCCTGCTCCTGAATACAGCTGACTGACATTGACTGTCTGT
GGAAAATGGGAGCTTGTGGAGAGCATAGTAATTTCAGAGAACTGAAGCCAAAAG
GATTAAAACCGCTGCTCTAAAGAAAAGAAAACTGGAGGCTGGCGCAGTGGCTCACGCC
TAATCCCAGAGGCTGAGGCAGGCGGTACACCTGAGGTCGGGAGTCGGGATCAGCCTGACCA
ACATGGAGAAACCCTACTGGAAAACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCAAAAAAAAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRVEW
KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNI PSSATIGNRAVLTCS EQDGSPPSE YTWFKD GIVMPTNPKSTRAFSNS
SYVLNPTTGE LVFDPLSASDTGEYSCEARNGYGT PMTSNAVRMEAVERNVGVIVAAVLVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGCTCTGGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCGCGAGCCCGCTTCCACCCCGACCTCTGCCCAAGGCCGAGGCCCGAGCTCAG
GCTCGTCCCACCCACCAAGTCCAGTGCAGCACCAGTGGCTTATGCGTCCCCCTCACCTGG
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCTGCCCTGCACCGCGTCA
GTGACTGCTCTGGGGAACTGACAAGAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA
CCCAGACTGTCCCAGCTCCAGCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCCGGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCACCTCTCAGGAATGCC
ACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCCCTCTGTGGGAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGGAAGCCAACTGCCCTATGGGTTATTGCAGCTGCTGCGGTGC
TCAGTGCAAGCCTGGTCACCGCCACCCCTCCTCTTGTCCCTGGCTCCGAGCCAGGAGCGC
CTCCGCCACTGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGTCAGAACAGAACAGAC
CTCGCTGCCTGAGGACAAGCAACTGCCACCCACCGTCACTCAGCCCTGGCGTAGCCGGACA
GGAGGAGAGCAGTGCGGATGGGTACCCGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGAGCTAGGATGGGAACCTGCCACAGCCAGAACAGAC
GGGCTGGCCCCAGGCAGCTCCAGGGGTAGAACGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCRDLD CSDGSDEEECRIEPCTQKGQC PPPGLPCPCTGVSDCSGGDKKL
RNCSRLA CLAGELRCTL SDDCIPLTWRC DGH PDCP DSS DELCGT NEIL PEGD ATT MGPPVT
LES VTS LRN ATT MGPPVT LES VPS VGNATSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCACCGCGTCCGGTCTCGCTCGCTCGCGCAGCGGGGGCAGCAGAGGTCGCCACAGATGCGG
GTTAGACTGGCGGGGGAGGAGGCGGAGGAGGGAAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTTATCATGGAATGAACCCGAGCAATG
GAGATGGATTCTAGAGCAGCAGCAGCAGCACACCTCAGTCCCCCAGAGACTCTG
GCCGTGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGCGGGTT
CGATGACCTCAAGTGTGCTGACCCCGCATTCCCGAGAATGGCTTCAGGACCCCCAGCG
GAGGGGTTTCTTGAAAGGCTCTGTAGCCGATTTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCCTAGGCTGGATCCAAGTGA
TAATTCCATCTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCAA
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTATGAAGGATTCAAGATCCGG
TACCCGACCTACACAATATGGTTTCATTATGTCGCGATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCGTGAGACCTCTAGCCTCTTAATGGCTATGTAAACATCTCTGAGC
TCCAGACCTCCTCCCGTGGGACTGTGATCTCCTATCGCTGCTTCCGGATTAAACTT
GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTGTCCAGCCCACCCGGTG
CCTTGCTCTGGAAGCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTCGTCT
GCCACCCGCGGCCCTGTGAGCGCTACAACCACGGAACGTGGTGGAGTTTACTGCGATCCT
GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCCCTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCCTGA
CCACGTGGAAGATTGTGGCGTTACGGCAACCAGTGTGCTGGTGTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGCCCTCCGGAG
TTCCAGCAGTGACCTGACTTTGTGGTAGACGGCGTCCCCGTATGCTCCGTCTATG
ACGAAGCTGTGAGTGGCGCTTGAGTGCCTTAGGCCCGGGTACATGGCCTCTGTGGGCCAG
GGCTGCCCTTACCCGTGGACGACCAGAGCCCCCAGCATAACCCGGCTCAGGGACACGGA
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTGAGCTGCTCCAAA
GTCTGTATTCACCTCCAGGTGCCAAGAGAGCACCCACCCCTGCTCGACAACCTGACATA
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCCAGGCATCCATCATGCCACTGGT
GTTGTTCTTAAGAAACTGATTGATTTAGACAAATGTAAACAA
ATACATGTTGATCTGTGGAGTTGATTCTTCTCTTGGTTAGACAAATGTAAACAA
AGCTCTGATCCTAAAATTGCTATGCTGATAGAGTGGTAGGGCTGGAAGCTGATCAAGTC
CTGTTCTTCTTGACACAGACTGATTAAAATTAAAAGNAAAAAA

FIGURE 48

MYHGMNPSNGDFLEQQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPIQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDTDTGPGESETCDS
VSGSSELLQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWVLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCACCGCGTCCGCTCCCGCCCTCCCCCGCCTCCCGTGCCTCCGTCGGCTGGCTAGAGA
TGCTGCTGCCCGGGTTGCAGTTGTCGCACGCCCTGCCGCCAGCCGCTCCACCGCCGT
AGCGCCCGAGTGTGCGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGAACCGCGTACAGG
CCGTGCTGCTGCCGTGCTGGTGGGCTGCCGCCGACGGTCGCCTGCTGAGTGCC
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCTGTTA
TAAAGTCATTACTTCCATGATACTTCTGAAGACTGAACCTTGAGGAAGCCAAGAAGCCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA
AAGTCATTGAAAACCTCTGCCATCTGATGGTACTCTGGATTGGCTCAGGAGGCCTGA
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTTGGACTGATGGCAGCATAT
CACAATTAGGAACTGGTATGTGGATGAGCCGTCTGCCAGCGAGGTCTGCGTGGTCATG
TACCATCAGCCATGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGATGATGA
CCGGTGCAACATGAAGAACAAATTTCATTGCAAATATTCTGATGAGAAACCAGCAGTCCT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAACACAG
GAAGAAGATGCCAAAAAAACATTAAAGAAAGTAGAGAACAGCTGCCTGAATCTGGCTACAT
CCTAATCCCCAGCATTCCCCTCTCCTCCTCTGTGGTACCCACAGTGTATGTTGGTTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCCTAGCACAAAGAACACACCATC
TGGCCCTCTCCTCACCAAGGAAACAGCCGGACCTAGAGGTCTACAATGTCTAACAGAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGCCAGACCTGAAGAATATTCAATTCCAGTGTGTT
CGGGAGAAGCCACTCCGATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGTTGTGACTCTGGTGGAGAGTGGATTGTGACCAATGACATTATGA
GTTCTCCCCAGACCAAATGGGAGGAGTAAGGAGTCTGGATGGTGGAAAATGAAATATATG
GTTATTAGGACATATAAAAACTGAAACTGACAACAAATGGAAAAGAAATGATAAGCAAATC
CTCTTATTTCTATAAGGAAATACACAGAACGGTCTATGAACAAAGCTTAGATCAGGTCTGT
GGATGAGCATGTGGTCCCCACGACCTCCTGTTGGACCCACGTTGGCTGTATCCTTAT
CCCAGCCAGTCATCCAGCTCGACCTTATGAGAACGGTACCTGCCAGGTCTGGCACATAGTA
GAGTCTCAATAATGTCACTTGGTTGGTGTATCTAACTTTAAGGGACAGAGCTTACCTG
GCAGTGATAAAAGATGGGCTGTGGAGCTTGGAAAACCACCTCTGTTTCTGCTCTACAG
CAGCACATATTATCATACAGACAGAAAATCCAGAACCTTTCAAAGCCCACATATGGTAGCACAG
GTTGGCCTGTGCATGGCAATTCTCATATCTGTTTTCAAAGAATAAAATCAAATAAGA
GCAGGAAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRGGTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSIESEDEQKLIKEFIENLLPSDGDFWIGLRRREEKQSNSTACQDL
YAWTDGSISQFRNWYDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNFICKY
SDEKPAVPSRREAEGEETELTPVLPETQEEDAKKTFKESREAALNAYILIPSIPLLLL
VTTVVCWVWICRKRKREQPDPSKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSSESGFVTLSVESGFVTNDIYEFS
PDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGAGGCACAGCGTCCCTGCTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTGGGGCGCCCGCTGAGCAGGGCCGGCCAGAAGACTTGT
GTTGCCTCCTGCAGCCTAACCCGGAGGGCAGCGAGGGCTACCACCATGATCACTGGTGT
GTTCAGCATGCGCTTGTGGACCCAGTGGCGTCTGACCTCGCTGGCGTACTGCCTGCACC
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCATGCCAGTGTCCGGTCAACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTGTTGACACCGGGCTGGAGTCCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCAAACTC
AGTTGATTACACAGTCACCAATCTAGCTGGTGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCAT
GCAGCAAATGTTGCCTGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTC
TTTCACCAACCTCAACCCACAGGAGGTCTTATTGTTCCACTAACATTTCGGAATCTG
GAGTCCACCCGTTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTCAAAGTCTTGTATCCAACTACCAAAGCTGGAGCCTGA
GGCAGAGAACCAAGAGGCCGGAGGCAGACTGCCTTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCAAGCTGCCCATGCTGAAGAGATTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTGTACATACTGCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCATTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTATGCGGCTCATGATG
TGACCTTCATACCGCTTTAATGACCCGGGATTTTGACCACAAATGGCCACCGTTGCT
GTTGACCTGACCATGGAACCTTACCAAGCACCTGGAATCTAAGGAGTGGTTGTGCAGCTCTA
TTACCAAGGGAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCGTGGACATGT
TCTTGAATGCCATGTCAGTTATACCTTAAGCCCAGAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACGTGATTATAAAAGCAGGATGTGTTGATT
TTAAAATAAAGTGCCTTATACAATG

FIGURE 52

MITGVFSMRLWTPGVVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLKKVKDRMGIDSSDKVD
FFILLDNVAAEQAHNLPSMPLKRFARMIEQRRAVDTSLYILPKEDRESLQMAVGPFHLILES
NLLKAMDSATAPDKIRKLYLYAAHDVTIFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMSVTLSPEKYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTAACATACTTGCAGCTAAACTAAATATTGCTGCTGGGGACCTCCTCTAGCCT
TAAATTCAGCTCATCACCTCACCTGCCTGGTCATGGCTCTGCTATTCTCCTGATCCTT
GCCATTGCAACCAGACCTGGATTCCCTAGCGTCTCCATCTGGAGTGCAGCTGGGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCAGTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGCCGGAGCTGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTATG
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTCTTCTCCCCA
GTCCCAGAGGGTGTCAAGGCTGGCTGACGCCCTGGCATTGCAAGGGACGCGTGGAAAGTGA
GCACCAGAACCAAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGCCGAAAGGTGG
TGTGCCGGCAGCTGGATGTGGAGGGCTGTACTGACTCAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCTCA
GGATTGCCCTCTGGCCTGGGGAAAGAACACCTGCAACCAGATGAAGACACGTGGTCG
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGCTCTGCTGTGATGACAACCTGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGCTGTGGGAAGTCCCTCTCCCTCCTCAGAGACCGGA
AATGCTATGCCCTGGGTTGCCGATCTGGCTGGATAATGTTGTTGCTCAGGGGAGGGAG
CAGTCCCTGGAGCAGTGCAGCACAGATTGGGGTTACGACTGCACCCACCAGGAAGA
TGTGGCTGTCATCTGCTCAGTGATGGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTACTGTCTACATGACTGCATGGATGAACACTGATCT
TCTTCTGCCCTGGACTGGACTTATACTTGGTGCCTGATTCTCAGGCCTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTCTCAGGCCATCAGACATAGTTGAACTACATCA
CCACCTTCCTATGTCTCCACATTGCACACAGCAGATTCCAGCCTCCATAATTGTGTGTAT
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACACATA
CACCAATTGTCCTGTTCTGTGAAGAACTCTGACAAAATACAGATTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTAAAGGATAAATTCTGAATTGGTATGGGTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACCTTATTACAATAATAAGATAGCAC
TATGTGTTCAA

FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGGHLRCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCQTGWSLRAAKVVCRLGCGRAVL
TQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCSGRLEVLHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACCGCGTCCGGACCGTGGCGGACCGTGGCCGGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCACAGCCATCCTGCCCTGCTGTTGGCTGCCCTGGG
CGTCTCGGCTCTCCGGCTGCTGCAGTGGGTGCGCGGGAAAGGCCTACCTGCGGAATGCTG
TGGTGGTGATCACAGGCGCACCTCAGGGCTGGCAAAGAATGTCAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGGCCGAATGGTGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC
TCACAGACTCTGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTGGCTATGTC
GACATACTTGTCAACAATGCTGGATCAGCTACCGTGGTACCATCATGGACACACCAGTGG
TGTGGACAAGAGGGTCATGGAGACAAACTACTTGGCCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGAGGAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCTTTGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTG
CTGTCTCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTGTAAATGCCATCACCGCGATGGATCTAGGTATGGAGTTATGGAC
ACCACCCACAGCCCAGGGCCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTGCTGCTGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCTGGCTGTTATCTCGAA
CTCTGGCTCCTGGCTCTTCTCAGCCTCATGGCCTCCAGGGCCAGAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTGAGACTTTAATGGAGATTGCTCACAAGTGG
AAAGACTGAAGAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATCAAAACGACAACA
AGCTTCTTCCCAGGGTGAGGGAAACACTTAAGGAATAATGGAGCTGGGTTAACACT
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAGGGCGGCCGACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGGTTATTGCAGCTATAATGGTTAC

FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVIITGATSGLGKECAKVFYAAAGA
KLVLICRNGGALEELIRELTASHATKVQTHKPVLVTFDLTDGAI
VAAAEEILQCFGYVDIL
VNNAGISYRGTIMDTTDVVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSIQGKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPV
EVAQDVLA
AVGKKKD
VILADLLPSL
AVYLRT
LAPGLFFSL
MASRARKER
KSKNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

CCACACGCGTCCGCTGGTGTAGATCGAGCAACCCCTAAAGCAGTTAGAGTGGTAAAAAA
AAAAAAAAACACACAAACGCTCGCAGCCACAAAAGGGATGAAATTCTTCTGGACATCCTC
CTGCTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTCGTGAAGCTTTTATTCTAA
GAGGAGAAAATCAGTCACCAGCGAAATCGTGTGATTACAGGAGCTGGCATGGAATTGGGA
GAATGACTGCCTATGAATTGCTAAACTAAAAGCAAGCTGGTCTCTGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTCATACCTTG
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTGTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTACTTGACACATTCTGGACTACAAA
GGCATTCTTCCTGCAATGACAAGAATAACCATGGCCATTGTCACTGTGGCTTCGGCAG
CTGGACATGTCTCGGTCCCCTTACTGGCTTACTGTTCAAGCAAGTTGCTGCTGTTGGA
TTTCATAAAACTTGACAGATGAACGGCTGCCTACAAATACTGGAGTCAAAACAACATG
TCTGTGTCCTAATTGTAACACTGGCTTCATCAAAATCCAAGTACAAGTTGGACCCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGATTCTGACTGAGCAGAAGATG
ATTTTTATTCCATCTCTATAGCTTTTAACACATTGGAAAGGATCCTGAGCGTT
CCTGGCAGTTAAAACGAAAATCAGTGTAAAGTTGATGCAGTTATTGGATATAAAATGA
AAGCGCAATAGCACCTAGTTCTGAAAACGATTTACCAAGGTTAGGTTGATGTCATCTA
ATAGGCCAGAATTAAATGTTGAACCTCTGTTCTAATTATCCCCATTCTCAATA
TCATTTGAGGCTTGGCAGTCTCATTACTACCACTGTTCTTAGCCAAAAGCTGATT
ACATATGATATAAACAGAGAAACCTTAGAGGTGACTTTAAGGAAAATGAAGAAAAGAA
CCAAAATGACTTATTAAAATAATTCCAAGATTATTGTTGCTCACCTGAAGGCTTGCAA
AATTGTAACATAACCGTTATTAAACATATATTATTGTTGATGCACTTAAATTGTTG
ATAATTGTTGTTCTTTCTGTTCTACATAAAATCAGAAACTCAAGCTCTAAATAAAA
TGAAGGACTATATCTAGTGGTATTCACAATGAATATCATGAACCTCTCAATGGTAGGTT
ATCCTACCCATTGCCACTCTGTTCTGAGAGATACCTCACATTCCAATGCCAACATTCT
GCACAGGGAGCTAGAGGTGGACACGTGTTGCAAGTATAAAAGCATCACTGGATTAAAG
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAATGGATCACACTTAAAAAAA
AAA
AAAAAAAAAAAAAAAAAAAAAAA

FIGURE 58

MKFLLDILLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAAKCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCACCGCGTCCGCGGACGCGTGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCGGCTC
AGGGAGGAGCACCGACTGCGCCGCACCCCTGAGAGAATGGTTGGTCCATGTGGAAAGGTGATTG
TTTCGCTGGCCTGTTGATGCCTGGCCCTGTGATGGCCTGTTCGCTCCCTATACAGAAGT
GTTCCATGCCACCTAACGGAGACTCAGGACAGCCATTATTCCTACCCCTTACATTGAAGC
TGGGAAGATCCAAAAGGAAGAGAATTGAGTTGGTCGGCCCTTCCCAGGACTGAACATGA
AGAGTTATGCCGGCTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTCTGGTTC
TTCCCAGCTCAGATAAGCCAGATGCCAGTAGTTCTCTGGCTACAGGGTGGCCGGG
AGGTTCATCATGTTGGACTCTTGTGGAACATGGCCTTATGTTGTACAAGTAACATGA
CCTTGCCTGACAGAGACTTCCCTGGACCACAAAGCTCTCCATGCTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTTACTGATGATAACCACGGATATGCAGTCATGAGGACGATGT
AGCACGGGATTATACAGTGCACTAATTCAAGTTTCCAGATATTCTGAATATAAAAATA
ATGACTTTATGTCACTGGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC
ATCCATTCCCTCAACCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA
TGGATATTCTGATCCGAATCAATTATAGGGGCTATGCAGAATTCTGTACCAAATTGGCT
TGTGGATGAGAAGCAAAAAGTACTTCCAGAAGCAGTGCATGAATGCATAGAACACATC
AGGAAGCAGAACTGGTTGAGGCCTTGAATACTGGATAAAACTACTAGATGGCGACTTAAC
AAGTGATCCTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTGCGGT
GCACGGAACCTGAGGATCAGCTTACTATGTGAAATTGGTCACTCCCAGAGGTGAGACAA
GCCATCCACGTGGGAATCAGACTTTAATGATGGAACTATAGTTGAAAAGTACTTGCAGA
AGATACAGTACAGTCAGTTAACGCCATGTTAACTGAAATCATGAATAATTATAAGGTTCTGA
TCTACAATGCCAACGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTGATGGC
ATGGACTGGAAAGGATCCCAGGAATACAAGAAGGCAGAAAAAAAGTTGGAAGATCTTAA
ATCTGACAGTGAAGTGGCTGGTACATCCGGCAAGCGGGTGACTTCCATCAGGTATTATTC
GAGGTGGAGGACATATTTCACCTATGACCAGCCTCTGAGAGCTTGACATGATTAATCGA
TTCATTATGGAAAAGGATGGGATCCTTATGTTGGATAAAACTACCTTCCAAAAGAGAACAT
CAGAGGTTTCATTGCTGAAAAGAAAATCGTAAAACAGAAAATGTCATAGGAATAAAAAAA
TTATCTTTCATATCGCAAGATTTTCATCAATAAAATTATCCTGAAACAAGTGAGC
TTTGTTTTGGGGGAGATGTTACTACAAAATTACATGAGTACATGAGTAAGAATTACA
TTATTAACTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAATGA
AATTAGGGTCTGAATAGGAAGTTAATTCTTAAGAGTAAGTGAAGTGCAGTTG
TAACAAACAAAGCTGTAACATCTTCTGCCAATAACAGAAGTTGGCATGCCGTGAAGGT
GTTGGAAATATTATTGGATAAGAATAGCTCAATTATCCCAAATAATGGATGAAGCTATAA
TAGTTTGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAACATTCTTGAAATA
AAAATATTATATAAAAGTAAAAAA

FIGURE 60

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDSGQPLFLTPYIEAGKIQKGRELSL
VGPPFPGLNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPyVVTTSNMTLDRDRFPWTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSLNPVREVKINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEIILDKLLDGDLTSDPSYFQNVTG
CSNNYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGQTFNDGTIVEKYLREDTVQSVKPWLT
EIMNNYKVLIYNGQLDIIVAALTERSLMGMDWKGSQEYKKAEEKVWKIFKSDSEVAGYIRQ
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTCCGGCTCCGAATGGCACATGTGGAATCCAGTCTTGGCTACAACAT
TTTCCCTTCTAACAGTTCTAACAGCTGTTAACAGCTAGTGATCAGGGTTCTTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTG
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGAGTGAGGTGATGGAAG
TCTAAAATAGGAAGGAATTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGAGGGCCTGCTAACAGCTTCAAAAAACAGGAGCGACTTCACTGGCTGGGAT
AAGACGTGCCGGTAGGGATAGGAAAGACTGGTTAGTCCTAACATCAAATTGACTGGCTGGG
TGAACCTCAACAGCCTTAAACCTCTCTGGAGATGAAAACGATGGCTTAAGGGCCAGAAA
TAGAGATGCTTGTAAAATAAAATTAAAAAGCAAGTATTTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATCCCTGAACATTCTAACAGAGGAGAAAGTATGTTAAAATA
GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGACCCCTGGGTC
AGGCCAGCCTTTGCTCCTCCGGAAATTATTGGTCTGACCACTCTGCCTTGTGTTT
GCAGAATCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCTGGAGGTGG
ACAGCCGCTCTGTGGTCTGCTCAGGGTCTGGGTGCTGCTGGCCCCCAGCAGCCGGC
ATGCCTCAGTCAGCACCTCCACTCTGAGAATCGTGAUTGGACCTTCAACCACCTGACCGT
CCACCAAGGGACGGGGCGCTATGTGGGGGCATCAACCGGGTCTATAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTCATAACAGACAGGGCAGAAGAGGACAACAAGTCTCGTACCCG
CCCTCATCGTGCAGCCCTGCAAGTGCTCACCTCACCAACAATGTCACAAAGCTGCT
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGAGCCTCTACCAGGGGTCTGCA
AGCTGCTGGGCTGGATGACCTCTTCATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC
CTGTCCAGTGTCAACAAGACGGCACCATGTACGGGTGATTGTGCGCTCTGAGGGTGAGGA
TGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCGACCTGTCCA
GCCGGAAGCTGCCCGAGACCCCTGAGTCCTCAGCCATGCTGACTATGAGCTACACAGCGAT
TTTGTCTCCTCTCATCAAGATCCCTCAGACACCCTGGCCCTGGTCTCCCACTTGACAT
CTTCTACATCTACGGCTTGCTAGTGGGGCTTGTCTACTTCTCACTGTCCAGCCGAGA
CCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTACACCTCACGCATCGTGG
CTCTGCAAGGATGACCCCAAGTTCACTCATACGTGTCCCTGCCCTCGGCTGCACCCGGG
CGGGGTGGAATACCGCCTCTGCAAGGCTGCTTACCTGGCCAAGCCTGGGACTCACTGGCC
AGGCCTCAATATCACCAAGCCAGGACGATGTACTCTTGCCTCTCCATCCGGGCATCAACTT
CAAGTATCACCAAGGGCCGATGACTCTGCCCTGTGTGCCTTCCATCCGGGCATCAACTT
GCAGATCAAGGAGCGCCTGCACTCTGCTACCAAGGGCGAGGGCAACCTGGAGCTCAACTGGC
TGCTGGGAAGGACGTCCAGTGCACGAAGGCGCTGCCCCATCGATGATAACTTCTGTGGA
CTGGACATCAACCAGCCCTGGAGGCTCAACTCCAGTGGAGGGCCTGACCCCTGTACACCAC
CAGCAGGGACCGCATGACCTCTGTGGCCTCTACGTTACAACGGCTACAGCGTGGTTTG
TGGGGACTAAGAGTGGCAAGCTGAAAAGGTAAGAGTCTATGAGTTAGATGCTCCAATGCC
ATTCACCTCCTCAGCAAAGAGTCCCTTGGAGGTAGCTATTGGTGGAGATTTAACTATAG
GCAACTTATTTCTGGGAACAAAGGTGAATGGGGAGGTAAGAAGGGGTTAATTGTG
ACTTAGCTTCTAGCTACTTCCTCCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA
TTCAATATTCCAAACTTAAGAAAAACTTAAGGAAGGTACATCTGCAAAAGCAAA

FIGURE 62

MGTLGQASLFAPPNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP
RALEVDSRSVVLLSVVVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
YKLTGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNNVNKLLIIDYSENRLLACGSL
YQGVCKLLRLDDLFIΛVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLPRDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFASGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP
GDSLAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSALCAFPIRAINLQIKERLQSCYQGEGN
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFGTKSGKLKKVRVYEFRCSNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

FIGURE 64

MTTWSLRRR PARTLGLLLL VVILGFLV LRRLDWSTL VPLRLR HRQL GLQAK GWNFM LEDST FW
I FGGSIHYFRVPREYWRDRLLKMKACGLNTLTTYVPWNLHEPERGKFDFSGNLDLEAFVLMA
AEIGLWVILRPGPYICSEMDLGGLPSWLLQDPGMRLRTTYKGFT EAVDLYFDHLM SRRVPLQ
YKRGGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRG IVELL TDNDK DGLSKGIVQGV LAT
INLQSTHELQ LTTFLFNVQGTQPKMVMEYWTGWFDSWGGPHNILD SSEVLKTVSAIVDAGS
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTAKYMKL RDFFGSISGIP
LPPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSF GYI LY
TSITSSGILSGHVHD RGQVFVNTV SIGFLDYKTTKIAVPLI QGYTVLRILVENRGRV NYGEN
IDDQRKGLIGNLYLNDSP LKNFRIYSLDMKKSFFQRFGLDKWXSLP EPTPLPAFFLGSLSIS
STPCDTFLKLEGWEKGVVFINGQNLGRYWNIGPQK TLYLPGPWLS SGINQVIVFEETMAGPA
LQFTETPHLGRNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGGGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGTGGACGGTCCCAGGACC
CTGGTGAGGGTTCTCTACTTGGCCTTCGGTGGGGTCAAGACGCAGGCACCTACGCCAAAGG
GGAGCAAAGCCGGGCTCGGCCCGAGGCCCCCAGGACCTCCATCTCCAATGTTGGAGGAATC
CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC
AAGAAGCTGTCCGTGCCCTCGTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCA
GGCAGACACTCGGTGTTGTAAGGGTCACTGACCGGTTCTCTAGACGGGGCC
CGTCCGCTATGTGTCGGCAGCCTGCACTACTTCGGGTACCGCGGGTGTGCTTGGCCGAC
CGGCTTTGAAGATGCGATGGAGCGGCCTCAACGCCATACAGTTTATGTGCCCTGGAACTA
CCACGAGCCACAGCCTGGGTCTATAACTTAATGGCAGCCGGACCTCATTGCCTTCTGA
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTTACATCTGTGCAGAG
TGGGAGATGGGGGTCTCCCATCCTGGTTGCTCGAAAACCTGAAATTCAAGAACCTC
AGATCCAGACTCCTGCCGAGTGGACTCCTGGTTCAAGGTCTGCTGCCCAAGATATATC
CATGGCTTATCACAATGGGGCAACATCATTAGCATTAGGTGGAGAATGAATATGGTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGCACTTGGCTGGCTCTCCGTGCACTGCTAGG
AGAAAAGATCTGCTTTCACACAGATGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
GACTCTATACCACTGTAGATTTGGCCAGCTGACAACATGACCAAAATCTTACCCCTGCTT
CGGAAGTATGAACCCATGGGCATTGGTAAACACTGAGTAACAGGGTGGCTGGATT
CTGGGGCAGAATCACTCCACACGGTCTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGC
TCAAGTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG
AATGGTGCCGATAAGAAGGGACGCTTCCTCGATTACTACCAGCTATGACTATGATGCACC
TATATCTGAAGCAGGGACCCCACACCTAACGTTTGCTCTCGAGATGTCATCAGCAAGT
TCCAGGAAGTTCTTGGACCTTACCTCCCCGAGCCCCAAGATGATGCTTGGACCTGTG
ACTCTGCACCTGGTGGCATTACTGGCTTCTAGACTTGTGCTTGGCCCCGGCAT
TCATTCAATCTTGCCTAACGACCTTGAGGCTGTCAAGCAGGACATGGCTCATGTTGACC
GAACCTATATGACCCATACCATTGGAGCCAACACCATTCTGGGTGCCAAATAATGGAGTC
CATGACCGTGCCTATGTGATGGGATGGGTGTTCCAGGGTGTGGAGCGAAATATGAG
AGACAAACTATTTTGACGGGAAACTGGGTCAAACACTGGATATCTGGTGGAGAACATGG
GGAGGCTCAGCTTGGGTCTAACAGCAGTGAACCTAACGGCCTGTGAAGCCACCAATTCTG
GGCAAACAACTCTAACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTGTGAAGTG
GTGGTTCCCTCCAGTTGCCAAAATGCCATATCCTCAAGCTCCTCTGGCCCCACATTCT
ACTCCAAAACATTCCAATTAGGCTCAGTTGGGACACATTCTATATCTACCTGGATGG
ACCAAGGGCCAAGTCTGGATCAATGGTTAACCTGGGCGGTACTGGACAAAGCAGGGGCC
ACAACAGACCCCTACGTGCCAAGATTCTGCTGTTCTAGGGAGCCCTCAACAAAATTA
CATTGCTGGAACCTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTGGATAAGCCTATC
CTCAATAGCACTAGTACTTGCACAGGACACATATCAATTCCCTTCAGCTGATACACTGAG
TGCCTCTGAACCAATGGAGTTAAGTGGGACTTGAAGGTAGGCCGGCATGGTGGCTCATGC
CTGTAATCCCAGCACTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAAGGACTTCAAGA
CCAGCCTGGCCAACATGGTGAACCCCGTCCACTAAAAATACAAAATTAGCCGGCGTG
ATGGTGGGCACCTCTAACCTCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTGAATCC
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTGCACCTCCAGCCTGGCTGACAGTGA
GACACTCCATCTCAAAAAAA

FIGURE 66

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE
YGSYRACDFSYMRHLAGLFRAALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF
TLLRKYEPHGPLVNSEYYTGWLDYWGQNHSTRSAVTKGLENMLKLGASVNMYMFHGGTNF
GYWNGADKKGRFLPITTSDYDAPISEAGDPTPKLFALRDVISKFQEVLGPLPPPSPKMML
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFLYRTYMTHTIFEPTPFWVPN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKKWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL
PGWTKGQVWINGFNLGRYWTQGPQQTLYVPRFLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSAADTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTTGAACACGTCTGCAAGCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC
ACCCACAATATGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT
TTATGGCTTATCTGCCTCTACACTCTTCTGGTTATTCAAGGATACCTTGAAGGAATATT
CTTCGAAAAAGTCAGAGAAGAGAGCAGTTAGTGACATTCCAGATGTCAAAACGATTT
GCGTTCCCTTCTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT
CTTGTCAAGAGTTAGTGAAAATAAACTTAGGGAAATTAGTTGAACCATGAGTGGACATTG
AAAAACTCAGGCAGCACATTCACGCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG
CTGTCGGGGGTGCCGATGCTGTCTTGACCTCACAGACCTGGATGTGCTAAAGCTTGA
AATTCCAGAAGCTAAAATTCTGCTAAGATTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCACTGAGA
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCTGCCTGGGTGTATTGCTCAAAAA
CCTTCGAGAGTTGTACTTAATAGGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTATAATGACGGCAC
TAAACTCTTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCCAGA
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTCTAATTACAGGAACGGAT
TTAAAGTCCAATAACATTGCAACAATTGAGGAATCATCAGTTCCAGCATTAAAACGACT
GAATTGTTAAAATTATGGATAACAAAATTGTTACTATTCCCTCCCTTATTACCCATGTCA
AAAACTTGGAGTCACTTTATTCTCTAACAAACAAGCTCGAACCTTACCAAGTGGCAGTATT
AGTTACAGAAACTCAGATGCTTAGATGTGAGCTACAACAACATTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTGCATATCACTGGAACAAAGTGGACATTCTGC
CAAACAAATTGTTAAATGCATAAAGTTGAGGACTTGAATCTGGACAGAACTGCATCACC
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG
CTTGGACCGCCTGCCAGCCAGCTGGGCCAGTGTGGATGCTCAAGAAAAGCGGGCTTGGT
TGGAAGATCACTTTGATAACCCTGCCACTCGAACGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCCTTGCAAATGGGATTAAAACTAAGATAATATGCACAGTGATGTGCAGGAAC
AACTCCTAGATTGCAAGTGCTACGTACAAGTTATTACAAGATAATGCATTAGGAGTAG
ATACATCTTTAAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTGTTAGGGTTAAGTCATTCCAAATCATTGTTTTAAATTGTTGTAACGGAT
AAAGGGAAGGAAAATTATAATCACTAATCTGGTTCTTTAAATTGTTGTAACGGAT
GCTGCCGCTACTGAATGTTACAAATTGCTGCCTGCTAAAGTAAATGATTAATTGACATT
TTCTTACTAAAAAAAAAAAAAA

FIGURE 68

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLRQHISRNAQDKQELHLFMLSG
VPDAVFDLTDLDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMICLQELRLKILHVKSNLTKVPSN
ITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAELELQNCELERIPHAIFSLSNLQELDLKS
NNIRTIEEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESLYFSNNKLES LPVAVFSLQ
KLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITS LP
EKVGQLSQLTQLELKGNCNDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCACGGCTCCGGCTTCTCTGGACTTGCATTCCATTCTTCACTGACAAACTGACTTTTTATTTCT
TTTTTCCATCTCTGGGCCAGCTTGGGATCCTAGGCCCTGGGAAGACATTGTGTTACACACATAAGGAT
CTGTGTTGGGTTCTCTCCTCCCTGACATTGGCATTGCTTAGGTACATCGAAGTCTTGACCTCATACTGATTATGCCTGTC
GCTCAGTGCTTGCACTTATCTGCCATTGCTAGGTACATCGAAGTCTTGACCTCATACTGATTATGCCTGTC
ATCGCTGGTGTATCCTGGCCCTTGCCTCTGCTGATAGTTGCTGCTCTGCTTTACTCAAAATACACAAC
GCGCTAAAAGCTGAAAGAACCTGAAGCTGTGGCTGTAAGGAACTACAACCCAGACAAGGTGTGGTGGCCAAG
AACAGCCAGGCCAAACATTGCCACGGAGTCTGCTGCCCTGCACTGCTGTGAGGTAGGAAAGGCTCCCTCTCAAA
AGTTTGATTCCCTGCCACCTTGCCTGCGACATAATGAGGGCTCTGAGTTAGGAAAGGCTCCCTCTCAAA
GCAGAGCCCTGAAGACTTCAATGATGTCAATGAGGCCACCTGTTGTGATGTGCAAGGCACAGAAGAAAGGCACAG
CTCCCCATCAGTTCATGGAAAATAACTCAGTGCTGCTGGGAACCAGCTGCTGGAGATCCCTACAGAGAGCTTC
CACTGGGGCAACCCCTCCAGGAAGGAGTTGGGGAGAGAGAACCCCTCACTGTTGGGAATGCTGATAACCCAGTCA
CACAGCTGCTCTATTCTCACACAAATCTACCCCTGCGTGGACTGACGTTCCCTGGAGGTGTCCAGAAA
GCTGATGTAACACAGAGCTATAAAAGCTGTCGGCTTAAGGCTGCCAGGCCCTGCCAAAATGGAGCTTGT
AGAAGGCTCATGCCATTGACCCCTCTTAATTCTCCTGTTGGCGGAGCTGACAATGGCGGAGGCTGAAGGCAAT
GCAAGCTGCACAGTCAGTCTAGGGGTGCCAATATGGCAGAGACCCACAAGCCATGATCTGCAACTCAATCCC
AGTGAGAACTGCACCTGGACAATAGAAAAGACCAGAAAACAAAGCATCAGAATTATCTTCTATGTCAGCTT
GATCCAGATGGAAGCTGTGAAAGTAAAACATTAAAGTCTTGACGGAACCTCCAGCAATGGCCTCTGCTAGGG
CAAGTCTGAGTAAAAGCACTATGTCCTGTATTGAATCATCATCAGTACATTGACGTTCAAATAGTTACT
GACTCAGCAAGAATTCAAAGAAACTGTCCTTGCTTCTACTACTTCTCTCTCTAACTCTCTATTCCAAACTGT
GGCGGTTACCTGGATACCTGGAGGATCCTTCAACAGCCCCAATTACCCAAAGCCGATCTGAGCTGGCTTAT
TGTGTTGGCACATACAAGTGGAGAAAGATTACAAGATAAAACTAAACTTCAAAGAGATTTCCTAGAAATAGAC
AAACAGTGCACATTGATTTCCTGCACTATGATGGCCCTCCACCAACTCTGCTGATGGACAAGTCTGT
GGCCGTGTGACTCCCACCTCGAATCGTCAACTCTCTGACTGTCGTTGCTACAGATTATGCCAATTCT
TACCGGGATTTCCTGCTTCTACACCTCAATTATGCAAGAAAACATCAACACTACATCTTAACTTGCTCTT
GACAGGATGAGAGTTATTATAAGCAAACTTCAACTAGAGGTTAACTCTAATGGGAAATAACTTGCAACTAAA
GACCCAACTTGCAGACCAAAATTATCAAATGTTGGAATTTCCTGTCCTCTTAATGGATGTGGTACAATCAGA
AAGGTAGAAGATCAGTCACATTACTACACCAATATAATCACCTTTCTGCATCTCAACTCTGAAGTGTACCC
CGTCAGAAACAACCTCCAGATTATGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATACATAACA
GAAGATGATGTAATACAAAGTCAAAATGCACTGGGCAAATAACACCCAGCATGGCTCTTTGAATCCAATTCA
TTTGGAAAAGACTATACTGAAATCACCATAATTATGTTGAACTTGAACCAAACCTTTTGTCAAGTTAGTCTGCAC
ACCTCAGATCCAAATTGGTGGTCTTGATACCTGAGGCCCTCCCACCTCTGACTTGCATCTCCAACC
TACGACCTAATCAAGAGTGGATGTAGTCAGAGATGAAACTTGTAAAGGTGATCCCTTATTGGACACTATGGGAGA
TTCCAGTTAATGCTTTAAATTCTGAGAAGTATGAGCTGTGATCTGCAGTGTAAAGTTGATATGTGAT
AGCAGTGGACCACCACTCGCTGCAATCAAGGTTGTGCTCCAGAAGCAAACGAGACATTCTCATATAATGG
AAAACAGATTCCATCATAGGACCCATTGCTGAAAAGGGATGAGAAGTGCAGTGGCAATTAGGATTCAGCAT
GAAACACATGCGGAAGAAACTCCAAACCAAGCCTTCAACAGTGTGCACTGTGTTCTCATGGTTCTAGCTG
AATGTGGTGAAGTGTAGCGACAATCACAGTGAGGCATTGAAATCAACGGGCAGACTACAAATACCAAGCTG
CAGAACTATTAACTAACAGGTCCAACCCATAAGTGAGACATGTTCTCCAGGATGCCAAAGGAATGCTACCTCGT
GGCTACACATATTGAATAATGAGGAAGGGCTGAAAGTGAACACACAGGCCTGCATGTA

FIGURE 70

MELVRRRLMPLTLLSCLAEILTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIRIIFSYVQLDPGSCESENIVFDGTSSNGPLLQVCSKNDYVPVFESSSTLT
FQIVTDSARIQRTVFVFYYFFSPNISIPNCGGYLDTLEGSFTSPNPKPHPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCGRTPTFESSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLCSSDRMRVIISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIIITFSASSTSEVITRQKQLQIIVKCEMGHNS
VEIYYITEDDVIQSQNALGKYNTSMALFESNSFEKTIILESPYYVDLNQTLFVQVSLHTSDPN
LVVFLLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYL
QCKVLICDSSDHQSRCNQGCVRSKRDIISSYKWKTDIIIGPIRLKDRSASGNQFQHETHA
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCCGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG
GGAC**ATG**CGGCCCGAGGAGCTCCCAGGCTCGCGTTCCCGTGTGCTGTTGCTGC
TGCTGCCGCCGCCGTGCCCTGCCACAGCGCCACGCCGCTCGACCCCACCTGGGAGTCC
CTGGACGCCGCCAGCTGCCCGTGGTTGACCAGGCCAAGTCGGCATCTTCATCCACTG
GGGAGTGTGTTCCGTGCCAGCTCGGTAGCGAGTGGTCTGGTGGTATTGGCAAAAGGAAA
AGATACCGAAGTATGTGGAATTATGAAAGATAATTACCCCTAGTTCAAATATGAAGAT
TTTGGACCACATTACAGCAAAATTGTTAATGCCAACAGTGGGCAGATATTTTCAGGC
CTCTGGTGCCAATACATTGTCTTAACCTCAAACATCATGAAGGCTTACCTGTGGGGGT
CAGAATATTCTGTGGAATGGAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCCTTGGACTGTACTATTCCCTTTGA
ATGGTTTCATCCGCTTCTGAGGATGAATCCAGTTATTCCATAAGCGGCAATTCCAG
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACTATCAGCCTGAGGTTCTGTGG
TCGGATGGTGACGGAGGAGCACCGGATCAAACTGGAACAGCACAGGCTTGGCCTGGTT
ATATAATGAAAGCCCAGTCGGGCACAGTAGTCACCAATGATCGTTGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTTCTATACCTGCAGTGATCGTTATAACCCAGGACATCTTGCCTA
CATAAATGGAAAAGTCATGACAATAGACAAACTGTCCTGGGCTATAGGAGGGAAGCTGG
AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTGTAGAGACAGTTCATGTG
GAGGAAATCTTGTATGAATATTGGGCCACACTAGATGGCACCATTTCTGTAGTTTGAG
GAGCGACTGAGGCAAGTGGGTCTGGCTAAAGTCATGGAGAAAGCTATTATGAAACCTA
TACCTGGCGATCCCAGAATGACACTGTCACCCAGATGTGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCCATTCTTCTTAAATGGCCCACATCAGGACAGCTGTTCTGGCCAT
CCCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAAC
GATTCTTGGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCAGATGC
CGTGTAAATGGGGCTGGCTAGCCCTAACTAATGTGATCTAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGTCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGTAAGAAACTGGATAAGAAAATTATTGGCAGTTGCCCTTCCCTTTCCACTA
AATTCTTCTTAAATTACCCATGTAACCATTAACTCTCCAGTGCACCTTGGCATTAAAGTC
TCCTCACATTGATTGTTCCATGTGTGACTCAGAGGTGAGAATTCTTACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAAGTGAAGGCAATATCCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGGATATTCTGGAAATGCATTGCTAGTCAT
TTTTTTGTGCCAACATCATAGAGTGTATTACAAAATCCTAGATGGCATAGCCTACTACA
CACCTAATGTGTATGGTATAGACTGTTGCTCTAGGCTACAGACATATACAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTGTATATCGAAACATATGGAAACATAGAGAAG
GTACAGTAAAATACTGTAAAATGGTCACCTGTATAGGGCACTTACCAAGAATGGAG
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA
TTGAACACTGCCAGACGTTATAAAACTGTATGCTTAGGCTACACTACATTATAAAAAAAA
GTTTTCTTCTTCAATTATAAAACATAAGTGTACTGTAACCTTACAAACGTTAATT
TTTAAAACCTTTGGCTCTTGTAAACACTTAGCTAAAACATAAAACTCATTGTGCAA
ATGTAA

FIGURE 72

MRPQELPRLAFPLLLLLLPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHWG
VFSVPSFGSEWFWWYWQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRGFLYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNYYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCCTCATATCACCAGTGGCCATC
TGAGGGTGTTCCTGGCTCTGAAGGGTAGGCACG**AT****GGCC**CAGGTGCTTCAGCCTGGTGTG
CTTCTCACTTCCATCTGGACCACGAGGCTCTGGTCAAGGCTCTTGCAGCAGAAGAGCT
TTCCATCCAGGTGTAGCAGAATTATGGGGATCACCCCTGTGAGCAGAAAAGGCGAACAGC
AGCTGAATTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGACTAAGTTGGCGGCAAG
GACCAAGTTGAAACAGCCTGAAAGCTAGCTTGAAACTGAGCTATGGCTGGTTGGAGA
TGGATTCTGTGGTCATCTCTAGGATTAGCCAAACCCCAAGTGTGGAAAAATGGGTGGGTG
TCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTGCAGCCTATTGTTACAACATCTGAT
ACTTGGACTAACTCGTCATTCCAGAAATTATCACCACCAAAGATCCCATTCAACACTCA
AACTGCAACACAAACAGAATTATTGTCAAGTGACAGTACCTACTCGGGGCATCCCCTT
ACTCTACAATACCTGCCCTACTACTACTCCCTGCTCCAGCTTCACTTCTATTCCACGG
AGAAAAAAATTGATTGTGTACAGAAGTTTATGAAACTAGCACCATGTCTACAGAAC
TGAACCATTGTTGAAAATAAAGCAGCATTCAAGAATGAAAGCTGCTGGTTGGAGGTGTCC
CCACGGCTCTGCTAGTGCTTGCCTCTTGGTGTGCAGCTGGTCTGGATTTC
TATGTCAAAAGGTATGTGAAGGCCTCCCTTTACAAACAAGAATCAGCAGAAGGAAATGAT
CGAAACCAAAGTAGTAAAGGAGGAAGGCCAATGATAGCAACCCATTAGAGGAATCAAAGA
AAACTGATAAAAACCCAGAAGAGTCAAGAGTCAAGCAAAACCTACCGTGCATGCCGGAA
GCTGAAGTT**AG**TGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTCATGCTCC
TTACCCCTGCCAGCTGGGAAATCAAAGGCCAAGAACCAAAGAACAGTCCACCCCTT
GGTCCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGC
CCTTCTCCTATTGTAACCCCTGTCTGGATCCTATCCTCACCTCAAAGCTTCCCACGGCC
TTCTAGCTGGCTATGCTTAATAATATCCCACGGAGAAGGAGTTGCAAAGTGC
GGACCTAAAACATCTCATCAGTATCCAGTGGTAAAAGGCCCTGGCTGTCTGAGGCTAGG
TGGTTGAAAGCCAAGGAGTCAGGACCAAGGCTTCTACTGATTCCGCAGCTCAGAC
CCTTCTCAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGCTCTTGAGCCGGTA
AGAGCAAAGAATGGCAGAAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATAACTGAG
ACCTAATCTCTGTAAGCTAAAATAAGAAATAGAACAAAGGCTGAGGATAAGACAGTACACT
GTCAGCAGGACTGTAAACACAGACAGGGTCAAAGTGTCTGAAACACATTGAGTTGGA
ATCACTGTTAGAACACACACACTTACTTTCTGGTCTCTACCACTGCTGATATTCT
AGGAAATATACTTTACAAGTAACAAAATAAAACTCTTATAAATTCTATTCTATCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTAAAAGTAATAAAATTCA
ACAAACATTGCTGAATAGCTACTATATGTCAGTGCAAGGTATTACACTCTGTAAT
TGAATATTATTCTCAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTCT
GTTTGATATTCTAGCTTACTTCCAAACTAATTCTATTGCTGAGACTAATCTT
ATTCAATTCTCTAATATGGCAACCATTATAACCTTAATTATTAAACACACCTAAGAAC
TACATTGTTACCTCTATATACCAAAAGCACATTAAAAGTGCCTAAACAAATGTACT
GCCCTCCTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTGACAAAAATTAA
AGCATTAGAAAACCTT

FIGURE 74

MARCFSLVLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNNPKCGKNGVGVLIWKPVSQF
AAWCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAALKNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGGCGGTCTGGCACCTCTAATTGCTCTCGTATTGGTGCCCGACTTCACGATGG
CTCGCCCAACCTTACTACCTCTGTCGGCCCTGCTCTGCTGCCTTCTACTCGTGAGGAA
ACTGCCGCCGCTCTGCCACGGTCTGCCACCCAACGCGAAGACGGTAACCGTGTGACTTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAGGCAACATTTCATGTTAGTAAAGTGGCAACACAAT
TCTTTCTTCCGCTTGGATATTGCATGGCCTACTTACATCACACTCTGCATAGTGTCC
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAACTAGAACGGGACAAGAGGGCACTTGGATTGTGGAGTTCTTGCAA
TTGGTCTAATGACTGCCAATCATTGCCCTATCTATGCTGACCTCTCCCTAAATACAAC
GTACAGGGCTAAATTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACCGGTAC
AAAGTGAGCACATCACCCTCACCAAGCAACTCCCTACCCTGATCCTGTTCCAAGGTGGAA
GGAGGCAATGGCGGCCACAGATTGACAAGAAAGGACGGCTGTCTCATGGACCTCTG
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATAACCAGCGGCCAAGAAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTCAACCCCCACCACAGTGTCA
TGGGAAAACAAGAAGGATAAATAAGATCCTCACTTGGCAGTGCTCCTCTCCTGTCAATT
CCAGGCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNATTNATGTTCCCTTGG
CTGNGACTGGNTGGGCAGCAGCTGAGCTTGTTAAAGAGGCATCTAGGGAATTGTCAG
GCACCCCTACAGGAAGGCCTGCCATGCTGTGGCCAAGCTTCACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGAAATGGTTCCCTCCAAGCTTGGGTAGTGTGTTACTGCTTATC
AGCTATTAGACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCATTCTCTTAG
TTGACCTGCACAGCTGGTAGACCTAGATTAAACCTAACGTAAGATGCTGGGTATAGAA
CGCTAACGAAATTTCACCCCAAGGACTCTGCTTCCTAACGCCCTCTGGCTTCGTTATGGTC
TTCATTAAAAGTATAAGCCTAACTTGTGCTAGTCCTAACGGAGAACCTTAACCACAAAG
TTTTTATCATTGAAGACAATATTGAACAAACCCCCCTATTGTGGGGATTGAGAACGGGTGAA
TAGAGGCTTGAGACTTCCCTTGTGTGGTAGGACTGGAGGAGAAATCCCTGGACTTCAC
TAACCCCTGACATACTCCCCACACCCAGTTGATGGCTTCGTAATAAAAGATTGGGATT
TCCTTTG

60
50
40
30
20
10

FIGURE 76

MAVLAPLIALVYSVPLSRWLAQPYYLLSALLSAAFLLVRKLPLCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

GGACAGCTCGGGCCCCGAGAGCTCTAGCCGTCGAGGAGCTGCCCTGGGACGTTGCCCTG
GGGCCCCAGCCTGGCCCGGTACCCCTGGCATGAGGAGATGGGCCTGTTGCTCCTGGTCCCA
TTGCTCCTGCTGCCCGGCTCCTACGGACTGCCCTCTACAACGGCTCTACTACTCCAACAG
CGCCAACGACCAGAACCTAGGCAACGGTACGGAAAGACCTCCTTAATGGAGTGAAGCTGG
TGGTGGAGACACCCGAGGAGACCCCTGTTCACCTACCAAGGGCCAGTGTGATCCTGCCCTGC
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCGCGCGTGTGCGTCAAATGGTGAAGCT
GTCGGAGAACGGGGCCCCAGAGAACGGACGTGCTGGCATCGGGCTGAGGCACCGCTCCT
TTGGGACTACCAAGGCCGCGTGCACCTGCGGCAGGACAAAGAGCATGACGTCTCGCTGGAG
ATCCAGGATCTGCGGCTGGAGGACTATGGCGTTACCGCTGTGAGGTATTGACGGCTGGA
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCGGGGTGGCTTCTTACCAAGTCCCCCA
ACGGCGCTACCAGTTCAACTTCCACGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCCGTG
GTGGCCTCCTTGAGCAGCTCTCCGGCCTGGAGGAGGGCCTGGACTGGTCAACGCCGG
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCGGCAGCCCTGCCGTGGCC
CAGGCCTGGCACCTGGCGTGCAGCTACGGCCCCGCCACGCCGCTGCACCGCTATGAT
GTATTCTGCTCGCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCTGAGAACGCT
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCCAAGGTGGAC
AGCTCTTGCCGCTGGAAGTTCCATGCCCTGGACCGCTGCGACGCTGGCTGGCTGGCAGAT
GGCAGCGTCCGCTACCCCTGTGGTTACCCGCATCTTAACGTGGCCCCCAGAGCCTGGGT
CCGAAGCTTGGCTTCCCCGACCCGAGAGCCGCTGTACGGTGTACTGCTACCGCCAGC
ACTAGGGACCTGGGCCCTCCCTGCCGATTCCCTCACTGGCTGTGTTATTGAGTGGTT
CGTTTCCCTGTGGGTTGGAGCCATTAACTGTTTATACTTCTCAATTAAATTCT
TTAACATTTTTACTATTTTGAAAGCAAACAGAACCCAATGCCCTCCCTTGCTCCTG
GATGCCCACTCCAGGAATCATGCTTGCCTCCCTGGCCATTGCGGTTTGTGGCTTCTG
GAGGGTTCCCGCCATCCAGGCTGGTCTCCCTCCCTTAAGGAGGTTGGTGCCCAGAGTGGC
GGTGGCCTGTCTAGAATGCCGCCGGAGTCCGGCATGGTGGCACAGTTCCCTGCCCT
CAGCCTGGGGAAAGAACGGCCTGGGGCTCCGGAGCTGGCTTGGCCTCTCCTGCC
CACCTCTACTCTCTGTGAAGCCGCTGACCCAGTCTGCCCACTGAGGGCTAGGGCTGGAA
GCCAGTTCTAGGCTTCCAGGCGAAATCTGAGGGAAGGAAGAAACTCCCTCCCCGTTCC
TCCCTCTCGGTTCAAAGAACCTGTTGTCATTGTTCTCCTGTTCCCTGTGTTGG
GGAGGGGCCCTCAGGTGTGTACTTGGACAATAATGGTGCTATGACTGCCCTCCGCCAA
AA
AA

FIGURE 78

MGLLLLVPLLLLPGSYGLPFYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEELDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSGPR
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCGGATGATGTGGCACCATCAGTTCTGCTGC
TTCTGTTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC
CAGGGGAGGGTGCACCAGCGCCCCCTGAGCGACGCTCCCCATGATGACGCCACGGGAA
CTTCCAGTACGACCATGAGGCTTCCTGGACGGGAAGTGGCCAAGGAATTGACCAACTCA
CCCCAGAGGAAAGCCAGGCCGTCTGGGGCGGATCGTGGACCGCATGGACCGCGGGGAC
GGCGACGGCTGGGTGTCGCTGCCAGCTTCGCGGTGGATCGGCACACGCAGCAGCGCA
CATACGGGACTCGGTGAGCGCCCTGGACACGTACGACACGGACCGGCAGGGCGTGTGG
GTTGGGAGGAGCTGCGCAACGCCACCTATGCCACTACGCCCTGGGACGAGCGGCTTCCGGGTGGC
CGACCAGGATGGGGACTCGATGCCACTCGAGAGGAGCTGACAGCCTCCTGCACCCCGAGG
AGTCCCTCACATGCCGGACATCGTATTGCTGAAACCCCTGGAGGACCTGGACAGAAACAAA
GATGGCTATGTCCAGGTGGAGGAGTACATCGCGATCTGTACTCAGCCGAGCCTGGGAGGA
GGAGCCGGCGTGGGTGCAGACGGAGAGGCAGCAGTCCGGACTTCCGGATCTGAACAAGG
ATGGGCACCTGGATGGGAGTGGAGGTGGCCACTGGGTGCTGCCCTGCCAGGACCAGCCC
CTGGTGGAAGCCAACCAACCTGCTGCACGAGAGCGACACGGACAAGGATGGCGGCTGAGCAA
AGCGGAAATCCTGGGTAAATTGGAACATGTTGTGGCAGTCAGGCCACCAACTATGGCGAGG
ACCTGACCCGGCACCGATGAGCTGTGAGCACCGCGCACCTGCCACAGCCTCAGAGGCCCG
CACAATGACCGGAGGAGGGCCGCTGTGGTCTGGCCCCCTCCCTGTCCAGGCCCGCAGGAG
GCAGATGCAGTCCCAGGCATCCTCTGCCCTGGCTCTCAGGGACCCCTGGTCGGCTTC
TGTCCCTGTACACCCCCAACCCCAGGGAGGGCTGTCAAGTCCCAGAGGATAAGCAATAC
CTATTCTGACTGAGTCTCCAGCCCAGACCCAGGGACCCCTGGCCCCAAGCTCAGCTCTAA
GAACCGCCCCAACCCCTCCAGCTCAAATCTGAGCCTCCACACATAGACTGAAACTCCCCT
GGCCCCAGCCCTCTCCTGCCTGGCTGGCCTGGGACACCTCCTCTGCCAGGAGGCAATAA
AAGCCAGCGCCGGACCTTGAAAAA
AAAAAAAAAAAAAAA
AAAAAAAAAAAAAAA

FIGURE 80

MMWRPSVLLLLLLLRHGAQGKPSPDAGPHQGRVHQAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTDGRVGWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ
FRDFRDLNKGHLDGSEVGHWVLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCTTGCCTCCGCACTCGGGCGCAGCCGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
GCGGGGGCGCGGGTGCAGGGATCCCTGACGCCCTGTCCCTGTTCTTGTGCTCCAG
CCTGTCGTCGTCGTTGGCCCCCGCTCCCCCGCGGTGCGGGGTTGCACACCGATCCTG
GGCTCGCTCGATTTGCCGCCAGGCGCCTCCAGACCTAGAGGGCGCTGGCCTGGAGCAG
CGGGTCGTCGTTGTCCTCTCCTCTGCCGCCGGGATCCGAAGGGTGCAGGGCTCT
GAGGAGGTGACGCCGGGCCTCCGCACCCCTGCCATTCTCCCTCTCCCAG
GTGTGAGCAGCCTATCAGTCAACCATGTCGCAAGCCTGGATCCCGCTCTGCCCTGGTGTG
TGTCTGCTGCTGCTGCCGGGCCGCGGGCAGCGAGGGAGCCGCTCCATTGCTATCACATG
TTTACCAAGGGCTGGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCAGGGGCTGCC
CTCTGAGGAATTCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG
GCTGCTGTCACAGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTATAGCCTACC
TGGTCGAGAAAATATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTTAGAT
GGTCTGCTTCTTCACAGTAACAAAGCAGGAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCCACAGCACATCCACCAACAGTAAACGACTAAAGAAAACACCCGAGAAGAAAATGG
CAATAAGATTGTAAGCAGACATTGCATTCTGATTGATGGAAGCTTAATATTGGCAGC
GCCGATTTAATTACAGAAGAATTGTTGGAAAAGTGGCTCTAATGTTGGAATTGGAACA
GAAGGACCACATGTGGGCCCTGTTCAAGCCAGTGAACATCCAAAATAGAATTTCAGTGA
AAACTTACATCAGCCAAAGATGTTTGTGCAATAAGGAAGTAGGTTCAGAGGGGTA
ATTCCAATACAGGAAAAGCCTGAAAGCATACTGCTCAGAAATTCTCACGGTAGATGCTGGA
GTAAGAAAAGGGATCCCCAAAGTGGTGGTATTATTGATGGTGGCCTCTGATGACAT
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTGGTGTCAATGTTAGTTCTGTGGCCA
AGCCTATCCCTGAAGAACTGGGGATGGTCAGGATGTCACATTGTTGACAAGGCTGCTGT
CGGAATAATGGCTTCTTCTTACACATGCCCAACTGGTTGGCACCACAAAATACGTAAA
GCCCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTTGAGCAAGACCTGTTATACT
CAGTGAACATTGCCCTCTAATTGATGGCTCCAGCAGTGGAGATAGCAATTCCGCCCTC
ATGCTTGAATTGTTCCAACATAGCCAAGACTTTGAAATCTGGACATTGGTGCAGAT
AGCTGCTGTACAGTTACTTATGATCAGCGCACGGAGTTCAAGTTCACTGACTATAGCACCA
AAGAGAATGTCCTAGCTGTCACTAGAAACATCCGCTATATGAGTGGTGGAACAGCTACTGGT
GATGCCATTCTTCACTGTTAGAAATGTTGGCCCTATAAGGGAGAGCCCCAACAGAA
CTTCCTAGTAATTGTCACAGATGGCAGTCCTATGATGATGTCAGGCCCTGCAGCTGCTG
CACATGATGCAGGAATCACTATCTCTGTTGGTGTGGCTGGCACCTCTGGATGACCTG
AAAGATATGGCTTCTAAACCGAAGGGAGTCTCACGCTTCTTCACAAGAGAGTTCACAGGATT
AGAACCAATTGTTCTGATGTCATCAGAGGCAATTGTTAGAGATTCTTAGAATCCCAGCAAT
AATGGTAACATTGACAACAGAAAGAAAAGTACAAGGGATCCAGTGTGAAATTGTATT
CTCATAACTGAAATGCTTACTGATGAAATCAGATACAAAATTAAGTATGTCAAC
AGCCATTAGGCAAATAAGCACTCCTTAAAGCCGCTGCCTCTGGTTACAATTACAGTGT
ACTTTGTTAAAACACTGCTGAGGCTTCATAATCATGGCTTTAGAAAATCAGGAAAGAGGA
GATAATGTGGATTAAAACCTTAAGAGTCTAACCATGCCTACTAAATGTACAGATATGCAAA
TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAAAAAAAA

FIGURE 82

MSAAWI PALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCPLEEFSVY
GNIVYASVSSICGAAVHRGVI NSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIQQRRLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLKNFTSAKDVLFAIKEVGFRGGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTFVDKAVCRNNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI
DGSSSVGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCCGCTCCGCACCCGGCCCGCCACCGCGCCGCTCCGCATCTGCACCCGAGCCC
GGCGGCCTCCGGGGAGCGAGCAGATCCAGTCGGGCCCGCAGCGCAACTCGGTCCAGTCG
GGGCGGCGGCTCGGGCGCAGAGCGGAGATGCAGCGGCTGGGGCACCCCTGCTGTGCCTGC
TGCTGGCGGGGGCGTCCCCACGGCCCCCGCGCCCGCTCGACGGCGACCTCGGCTCCAGTC
AAGCCGGCCGGCTCTCAGCTACCGCAGGAGGAGGCCACCTCAATGAGATGTTCCGCGA
GGTTGAGGAAGTGGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTACCTCCCAGCTAT
CACAATGAGACCAACACAGACAGAAGGTTGAAATAATACCATCCATGTGCACCGAGAAAT
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTCAGAGACAGTTATCACATCTG
TGGGAGACGAAGAAGGCAGAAGGAGCCACGAGTCATCATCGACGAGGACTGTGGGCCAGC
ATGTAAGTGCAGTTGCCAGCTTCCAGTACACCTGCCAGCCATGCCAGGGCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGCAGTGGAGACCAAGCTGTGACAAACCAGAGGGACTGCCAGCGGGGCTG
TGCTGTGCCCTCCAGAGAGGCCCTGCTGTTCCCTGTGTGCACACCCCTGCCCGTGGAGGGCGA
GCTTGCCATGACCCGCCAGCCGGCTCTGGACCTCATCACCTGGAGCTAGAGCCTGATG
GAGCCTGGACCGATGCCCTGTGCCAGTGGCCTCTGCCAGCCCCACAGCCACAGCCTG
GTGTATGTGCAAGCCGACCTCGTGGGGAGCCGTGACCAAGATGGGAGATCCTGCTGCC
CAGAGAGGTCCCCGATGAGTATGAAGTGGCAGCTTATGGAGGGAGGTGCCAGGAGCTGG
AGGACCTGGAGAGGGCCTGACTGAAGAGATGGCGCTGGGGAGCCTGCCGTGCCCGCT
GCACTGCTGGAGGGGAAGAGATTTAGATCTGGACCAGGCTGTGGTAGATGTGCAATAGAA
ATAGCTAATTATTCCCAGGTGTGCTTAGGCGTGGCTGACCAGGCTTCTTACA
TCTTCTTCCCAGTAAGTTCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTGTTCA
TCCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGCTGGAGAGTCAGGCAGGGTTAAC
TGCAGGAGCAGTTGCCACCCCTGTCCAGATTATTGGCTGCTTGCCTCTACAGTTGGCAG
ACAGCCGTTGTTCTACATGGCTTGATAATTGTTGAGGGAGGAGATGGAAACAAATGTGG
AGTCCTCTCTGATTGGTTGGGAAATGTGGAGAAGAGTGCCTGCTTGCAAACATCAA
CCTGGAAAAATGCAACAAATGAATTTCACGCAGTTCTTCCATGGCATAGGTAAGCTG
TGCCTTCAGCTGTTGCAGATGAAATGTTCTGTTCACCCCTGCATTACATGTGTTATTCA
AGCAGTGTGCTCAGCTCTACCTCTGCCCCAGCAGCATTTCATATCCAAGATCAATT
CCTCTCTCAGCACAGCCTGGGGAGGGGTCAATTGTTCTCTCGTCCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTGCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTCT
CTGGTTGTGACTCTAACGCTCAGTGCCTCTCCACTACCCACACCAGCCTGGTGCCACCAA
AAGTGCTCCCCAAAAGGAAGGAGAATGGGATTCTTGAGGCATGCACATCTGGAATTAG
GTCAAACATTCTCACATCCCTCTAAAGTAACACTGTTAGGAACAGCAGTGTCTCAC
AGTGTGGGGCAGCGTCTTCTAACGACAATGATATTGACACTGCTCCCTTTGGCAGT
TGCATTAGTAACCTTGAAAGGTATATGACTGAGCGTAGCATACAGGTAACCTGCAGAAACA
GTACTTAGTAATTGTAGGGCGAGGATTATAAATGAAATTGCAAACACTAGCAGCAAC
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGAAACATGGTT
GTAATATGCACTGCGAACACTGAACTCTACGCCACTCCACAAATGATGTTTCAGGTGTCA
TGGACTGTTGCCACCATGTATTCCAGAGTTCTTAAAGTTAAAGTTGCACATGATTGTA
TAAGCATGCTTCTTGAGTTAAATTATGTATAAACATAAGTGCATTAGAAATCAAGC
ATAAATCACTCAACTGCAAAAAAAAAAAAAAA

FIGURE 84

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEEAAKASSEVNLPPSYHNETNTDKVGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRSECCG
DQLCVWGHCTKMATRGSGNTICDNQRDCQPGCCAFQRGLLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV
GSFMEEVQRQELEDLERSLTEEMALGEPAAAAALLGEEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 85

FIGURE 86

MRLLVAPLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA
VPPALPAGTQTLLLQNSIVRDQSELGYLANLTELDLSQNSFSDARCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLSNLLRAIDSRWFE
MLPNLEIILMIGGNKVDAILDMNFRPLANLRSVLVLAGMNLREISDYALEGLQSLSFYDNQ
LARVPRRALEQVPGLKFLDLNKNPLQRVPGDFANMLHLKELGLNNMEELVSIDKFALVNLP
ELTKLDITNNPRLSFIHPRAFHHLQPQMETLMLNNNALSALHQQTVESLPNLQEVGLHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPSLQ
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEGTLELRRVTAAEAGLYT
CVAQNLVGVADTKTVVVGRALLQPGRDEGQGLELRVQETHPYHILLSWVTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLLAAGLA AHLGTQPRKGVGGRPLPPAWAFWGWSAPSVRVV
SAPLVLPWNPGRKLPRSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

GCAAGCCAAGGCCTGTTGAGAAGGTGAAGAAGTCCGACCCATGTGGAGGAGGGGACATTGTGTACCGCCT
CTACATGCGGCAGACCATCATCAAGGTGATCAAGTTCATCTCATCATCTGCTACACCGTCTACTACGTGCACAA
CATCAAGTTGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCACCC
CCTGCCACACTCTCAAGATCCTGGCTCCTCTACATCAGCCTAGTCATCTCTACGGCTCATCTGCATGTA
CACACTGTGGTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTGAGTCGATCCGTGAGGAGAGCAGCTACAG
CGACATCCCCGACGTCAAGAACGACTTCGCGCTCATGCTGCACCTCATGACCAATACGACCCGCTACTCCAA
GCGCTTCGCCGCTTCTCGAGGTGAGTGAAGAACAGCTGCCAGTGAACCTCAACAAACGAGTGGACGCT
GGACAAGCTCCGGCAGCGGCTCACCAAGAACGCGCAGGACAAGCTGGAGCTGACCTGTTCATGCTCAGTGGCAT
CCCTGACACTGTGTTGACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCCCGCC
CAGCATTGCCAGCTCACGGGCCTCAAGGAGCTGTGGCTCTACCACACAGCGGCCAAGATTGAAGCGCCTGCGCT
GGCCTTCCTGCGCAGAACCTGCGGGCCTGCACATCAAGTTCACCGACATCAAGGAGATCCCCTGTGGATCTA
TAGCTGAAGACACTGGAGGAGCTGCACCTGACGGCAACTGAGCGGGAGAACACCGCTACATGTCATG
CGGGCTCGGGAGCTAACGCCTCAAGGTGCTCGGCTCAAGAGCAACCTAACGAAGCTGCCACAGGTGGTCAC
AGATGTGGCGTGCACCTGCAGAAGCTGTCATCAACAAATGAGGGCACCAAGCTCATCGTCTCAACAGCCTCAA
GAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCCACCTGGAGCGCATCCCCACTCCATCTTCAGCCT
CCACAACCTGCAGGAGATTGACCTCAAGGACAACAAACCTCAAGACCATCGAGGAGATCATCAGCTCCAGCACCT
GCACCGCCTCACCTGCCCTAACGACTGTCGCTGAGGAGCTGGGAGGAGCTGGGAGGAGCTGGGAGGAGCTGGGAGG
CCTGGAGCGCCTTACCTGAACCGAACAGATCGAGAAGATCCCCACCCAGCTTCTACTGCCGAAGCTGCG
CTACCTGGACCTCAGCCACAACAAACCTGACCTTCCCTGCCACATCGGCCCTCTGCAGAACCTCCAGAACCT
AGCCATCACGGCAACCGGATCGAGACGCTCCCTCCGGAGCTTCCAGTGCAGGAGCTGCCAGATCGCAGATCGAGCTGGGG
GGGCAACAACGTGCTGCAGTCAGTGCCTCCAGGGTGGCGAGCTGACCAACCTGACGAGATCGAGCTGGGG
CAACCGCTGGAGTGCTGCCGTGGAGCTGGCGAGTGCCACTGCTCAAGCGCAGCGGCTTGGTGGAGGA
GGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCTGAGCGAG
GCCGCCAGCACAGCAAGCAGCAGGCCAGGACAGCCTGCCGCTGGCAGGGAGCCTGGGCGCTGTGAGTCAGGCCAGAGCGAGA
AACTCCCGGACAGCCAGGACAGCCTGCCGCTGGCAGGGAGCCTGGGCGCTGTGAGTCAGGCCAGAGCGAGA
GGACAGTATCTGTGGGCTGGCCCTTTCTCCCTCTGAGACTCACGTCCCCCAGGGCAAGTGCCTGTGGAGGAG
AGCAAGTCTCAAGAGCGCAGTATTGGATAATCAGGGCTCTCCCTGGAGGGCAGCTCTGCCCAAGGGCTGAG
CTGCCACCAGGGCTGGGACCTCACTTTAGTTCTGGTATTATTCTCCATCTCCACCTCCTCATCC
AGATAACTTACATTCCCAGAAAGTTCAGCCAGATGGAAGGTGTTAGGGAAAGGTGGCTGCCCTTCC
TTGTCTTATTAGCGATGCCGCCGGCATTTAACACCCACCTGGACTTCAGCACAGTGGTCCGGGGCGAACAG
CCATGGGACGGTCACCCAGCAGTGCCGGCTGGCTCTGGCTGCCACGGAGAGCAGGCCAGCTGG
AAGGCCAGGCCCTGGAGCTTGCCCTCTCAGTTTGTGGCAGTTTAGTTTTGGTTTTTTTAATCAA
AAACAATTTTTAAAAAAAGCTTGGAAAATGGATGGTTGGGTATTAAGGAAAGGAAACTTAAAAAA
AAAAGACACTAACGCCAGTGAGTTGGAGTCTCAGGGCAGGGTGGCAGTTCCCTGAGCAAAGCAGCCAGACGT
TGAACGTGTTCTTCCCTGGCGCAGGGTGCTTCCGGATCTGGTGTGACCTGGTCCAGGAGTT
CTATTGTTCTGGGAGGGAGTTTTGTGTTGTTGGTTTTGGTTTTGGTGTCTGTTCTTCTCCTCC
ATGTGTCTTGGCAGGCACTCATTCGTGGCTGCGGCCAGGGAAATGTTCTGGAGCTGCCAAGGAGGGAGGAG
ACTCGGGTTGGCTAATCCCCGATGAACGGTGTCCATTGCCACCTCCCTCGTCGCCCTGCCCTCCA
CGCACAGTGTAAAGGAGCCAAGAGGCCACTTCGCCAGACTTGTGTTCCCCACCTCCTGCCATGGTGT
CCAGTGCCACCGCTGGCCTCCGCTGCTTCCATCAGCCCTGTCGCCACCTGGCTTCTCATGAAAGAGCAGACACTTA
GAGGCTGGTGGAGGAATGGGAGGTGCGCCCTGGAGGGCAGGCAGTGGTCCAGGCCGTTCCCTGGCGC
CTGGAGTGACACAGCCAGTCGGCACCTGGTGGCTGGAGGCCAACCTGCTTGTGTTAGACTCAC
CTGGTCCGGTCCCCACCTGGTGGCTGCTTGTGTTAGAGTCTCTGTCTTAATGATTATGT
CCATCCGTCTGCGTCCATTGTGTTCTGCGTGTGCTTGTGTTAGGATATAATCCTCAGAAATAATGCACACTAG
CCTCTGACAAACCATGAAGAAAAATCGTTACATGTGGGTCTGAACCTGTAGACTCGGTACAGTATCAAATAAA
ATCTATAACAGAAAAAA

FIGURE 88

MRQTIIKVIKFILIIICYTVYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRLQLNLNNEWTLDKLQRQLTKNAQDKLELHLFMLSGIPDTVFDLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLRENLRALHIKFTDIKEIPLWI
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHISIFSLHNLQEIDLKDNNLKTIEIIISFQ
HLHRLTCLKLWYNHIAYIPIQIGNLTNERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRALHGNNVLQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGACTGCGGCCTCTCCCGT
CCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGGGCCTGAACGCAGGAGCTGTCAATTGACT
GGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACCTCTCAGAACTGCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCAGGTTCTAGCACTGGATTGGAAACTTGAGGAAATTGGC
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTT
GTGGATAATCCCGTGGGCACTGGGTTCAAGTATGTGAATGGTAGTGGTGCCTATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTCTTCAGTTGCCACAAAG
AATTCCAGACAGTTCCATTCTACATTTCTCAGAGTCCTATGGAGGAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTATAAGGCCATTCAAGCAGGGACCATCAAGTGCACACTTGCGGGGGT
TGCCTGGGTGATTCCCTGGATCTCCCTGGTATTGGTCTCTCCTGGGGACCTTACCTGT
ACAGCATGTCTCTCGAAGACAAAGGTCTGGCAGAGGTGTCAAGGTTGCAGAGCAAGTA
CTGAATGCCGTAAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAACATCTTAACACTAAAGCACTCCCA
CGTCTACAATGGAGTCGAGTCTAGAATTCAACACAGGCCACCTAGTTGTCTTCAGCGC
CACGTGAGACACCTACAACGAGATGCCCTAACGCCAGCTCATGAATGGCCCCATCAGAAAGAA
GCTAAAATTATTCCCTGAGGATCAATCCTGGGAGGCCAGGCTACCAACGTCTTGTAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTGAGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATAACATGGTCAGGAGGCCTG
GGTGGAAACTGAAGTGGCCAGAACTGCCCTAAATTCAAGTCAGCTGAAGTGGAAAGGCCCTGT
ACAGTGACCCCTAAATCTTGAAACATCTGCTTTGTCAAGTCCTACAAGAACCTTGCTTTC
TACTGGATTCTGAAAGCTGGTCATATGGTTCTCTGACCAAGGGACATGGCTCTGAAGAT
GATGAGACTGGTGACTIONAGAAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTCCCTGTATCT
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAAGGCTCTGCAGAGGATAAAATCATTGTCTCT
GGAGGCAATTGGAAATTATTCTGCTTAAAAAAACCTAAGATTTTAAAAAAATTGAT
TTGTTTGATCAAAATAAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEIGPLSDLKPRKTTWLQAASLLFVDNPVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPVDVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNKGLYRE
ATELGKAEMIIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKIIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLKWPELPKFSQLWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP
SDQGDMALKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGCGCGCGCGGGCGCTGCTGCTGGCGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCCGCGCCGTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTGCGCATCGTGGGTGGAGAGGGACGCCGACTCGGGCGTTGGCCGTGGCA
GGGGAGCCTGCGCTGTGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCCTGGG
CACTCACGGCGGCGCACTGCTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTCGTATCGAATATCTATCTGAGCCCTGCTACCTGGGAATTCACCCATGACATTG
CCTTGGTGAAGCTGTGCACCTGTACACTAAACACATCCAGCCCATCTGTCTCCAG
GCCTCCACATTGAGTTGAGAACCGGACAGACTGCTGGTGACTGGCTGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCAGGTGCCATCATAAACAA
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCCGCAAGGACATCTTGGAGACATG
GTTTGTGCTGGCAACGCCAAGGCGGGAGGATGCCTGCTCGGTGACTCAGGTGGACCCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG
GTCGGCCAATCGGCCGGTGTACACCAATATCAGCCACCAACTTGAGTGGATCCAGAAG
CTGATGGCCAGAGTGGCATGTCCCAGCCAGACCCCTGCCACTACTCTTTCCCTCT
TCTCTGGCTCTCCACTCCTGGGCCGGTCTGAGCCTACCTGAGCCCATGCAGCCTGGGC
CACTGCCAAGTCAGGCCCTGGTCTCTGTCTTGTGTTGGTAATAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTCTCAAAAAAAAAAAAAAAAAAAAAAA

160
150
140
130
120
110
100
90
80
70
60
50
40
30
20
10

FIGURE 92

MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLW
DSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEJVQAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSWVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCACACGCGTCCGGACCGGTGGAGGGCAGAATGGACTCCAAGCCTGCCTCCTAGGGCT
CTTGCCCTCATCCTCTGGCAAATGCAGTTACAGCCCCGAGCCGACCAGCGGAGGACGC
TGCCCCCAGGCTGGGTGCCCCCTGGGCCGTGGGACCCCTGAGGAAGAGCTGAGTCTCACCTT
GCCCTGAGACAGCAGAAATGTGGAAAGACTCTCGGAGCTGGTGCAGGCTGTGCGGATCCCAG
CTCTCCTCAATACGGAAAATACCTGACCCCTAGAGAATGTGGCTGATCTGGTGGAGGCCATCCC
CACTGACCCCTCCACACGGTGCAAAATGGCTCTTGGCAGCCGGAGCCAGAAGTGCCATTCT
GTGATCACACAGGACTTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC
TGGGGCTGAGTTCATCACTATGTGGGAGGACCTACGGAAACCCATGTTGTAAGGTCCCCAC
ATCCCTACCAGCTTCCACAGGCCTGGCCCCCATGTGGACTTTGTGGGGGACTGCACCGT
TTTCCCCAACATCATCCCTGAGGCAACGTCTGAGCCGAGGTGACAGGGACTGTAGGCCT
GCATCTGGGGGTAACCCCCCTGTGATCCGTAAGCGATAACAACTTGACCTACAAGACGTGG
GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCCCTGGAGCAGTATTCCATGAC
TCAGACCTGGCTCAGTCATGCGCCTCTCGGTGGCAACTTGACATCAGGCATCAGTAGC
CCGTGTGGTTGGACAAACAGGGCCGGGCCGGGATTGAGGCCAGTCTAGATGTGCAGT
ACCTGATGAGTGGCTGGTGCACATCTCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG
GGACAGGAGCCCTCCTGCAGTGGCTCATGCTGTCAGTAATGAGTCAGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCCTACATCCAGCGGGTCA
ACACTGAGCTCATGAAGGCTGCCGCTGGGTCTCACCCCTGCTCTGCCCTCAGGTGACAGT
GGGGCCGGGTGGTCTGTCTGGAAAGACACCAGTTCCGCCAACCTCCAGGAACCTTCCATCACAAATGAAA
CCCCATGTCAACCACAGTGGGAGGCACATCCTCCAGGAACCTTCCATCACAAATGAAA
TTGTTGACTATATCAGTGGTGGCTCAGCAATGTGTTCCACGGCCTTCATACCAGGAG
GAAGCTGTAACGAAGTTCTGAGCTCTAGCCCCACCTGCCACCATCCAGTTACTTCATGC
CAGTGGCCGTGCCTACCCAGATGTGGCTGCACCTCTGATGGCTACTGGGTGGTCAGCAACA
GAGTGCCCATCCATGGGTGTCGGAACCTCGGCCTCTACTCCAGTGTGTTGGGGGATCCTA
TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCCCTTGGCTTCTCAACCCAAG
GCTCTACCAGCAGCATGGGCAGGTCTTGATGTAACCCGTGGCTGCCATGAGTCCTGTC
TGGATGAAGAGGTAGAGGGCCAGGGTTCTGCTCTGGCTGGATCCTGTAACAGGC
TGGGGAACACCAACTTCCAGCTTGCTGAAGACTCTACTCAACCCCTGACCCCTTCATC
AGGAGAGATGGCTTGTCCCCTGCCCTGAAGCTGGCAGTTCACTCCCTATTCTGCCCTGTTG
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTATCTCCCTAACCCGAA
TGCTGTGAGCTTGACTGACTCCAAACCCCTACCATGCTCCATCATACTCAGGTCTCCCTACT
CCTGCCCTAGATTCTCAATAAGATGCTGTAACTAGCATTTTGAAATGCCCTCTCCCTCCGC
ATCTCATCTTCTCTTCAATCAGGCTTCAAAAGGGTTGTATACAGACTCTGTGCACTA
TTTCACTTGATATTCAATTCCCAATTCACTGCAAGGAGACCTCTACTGTCACCGTTACTCT
TTCCCTACCCCTGACATCCAGAAACAATGGCCTCCAGTGCATACCTCTCAATCTGTTATG
GCCTTCCATCATAGTGCCCACCTCCCTCCTACTTAGCTTCCAGGTCTAACTTCTCTG
ACTACTCTTGCTTCTCCCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTTCATTGC
TCCATTGTAGATTTGCTTCTCAGTTACTCATTGCCCCCTGGAACAAATCACTGACA
TCTACAACCATTACCATCTCACTAAATAAGACTTTCTATCCAATAATGATTGATAACCTCAA
TGTAAAAAA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYGKYLTLENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL
SIRQAELLPGAEFHYYVGGPTETHVVRSPHYQLPQALAPHVDFVGGLHRFPPTSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLLFASGDGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHESDLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GGCGCGCGCTCTCTCCGGCCCCACACCTGTCTGAGCGCGCAGCGAGCCCGGGCCGGC
GGGCTGCTCGCGCGAACAGTGCTCGCATGGCAGGGATTCCAGGGCTCCTCTTCTC
TTCTTCTGCTCTGTGCTGTTGGCAAGTGAGCCCTACAGTGCCCCCTGAAACCCACTTG
GCCTGCATAACCGCTCCCTGTCGTCTGCCCAAGTCTACCCCTAATTAAGCCAAGCCAGACT
TTGGAGCCGAAGCAAATTAGAAGTATCTTCTCATGTGGACCCAGTGTCAAGGAACT
CCACTGCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG
CAGCCGCACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC
ACCGAGACTCAGGGTCTCAGGAAAGTCTCGAAGGAAGCGGCAGATTATGGCTATGACAGC
AGGTTCAGCATTGGAGGACTTCTGCTCAACTACCCCTTCAACATCAGTGAAGTT
ATCCACGGGCTGCACCGGCACCCCTGGTGGCAGAGAACGATGTCCTCACAGCTGCCACTGCA
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAACGCTTCGAGTGGCTTCTAAAGCCC
AAGTTAAAGATGGTGGTCGAGGGGCCAACGACTCCACTTCAGCCATGCCAGCAGATGAA
ATTCAGTGGATCCGGGTGAAACGCACCCATGTGCCCAAGGGTTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCTGGAACTCAAAAGCCCCACAAGAGAAAA
TTTATGAAGATTGGGTGAGCCCTCCTGCTAACGAGCTGCCAGGGGCCAGGGTCTGGGTCTAT
TGGTTATGACAATGACCGACCAGGAATTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA
CCTATGACTTGCTCTACCAGCAATGCGATGCCAGCCAGGGGCCAGGGTCTGGGTCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAACGAGTGGAGCGAAAATTATTGGCATTTCAGG
GCACCAGTGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAGAACACTC
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGGG
TGACACAGTGTCCCTGGCAGCAATTAAAGGTCTTCATGTTCTTATTAGGAGAGGCC
AAATTGTTTTGTCTGGCGTGCACAGTGTGTGTGTGTGTGTGTAAAGGTGT
CTTATAATCTTTACCTATTCTTACAATTGCAAGATGACTGGCTTACTATTGAAAATG
GTTTGTGTATCATATCATATCATTAAAGCAGTTGAAGGCATACTTTGCATAGAAATAA
AAAAAAACTGATTGGGCAATGAGGAATTGACAATTAAAGTTAATCTCACGTTTG
CAAACTTGATTTCATCTGAACCTGTTCAAAGATTATTAATATTAAATATTGGCATA
CAAGAGATATGAAAAA

FIGURE 96

MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVLPQSTLNLA
KPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSSGKS
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLS
TGCTGTLVAEKHVLTAACIHDGKTYVKG
TQKLRVGFLKPKFKDGGRGANDSTS
SAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYA
LLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCD
AQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATGCCCTGGTCTCTGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCCATGGTGGTTT
CTGGAGCGCCCCAGCCTGGTGGGGCTGTCTGGCACCTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATAACCTGTTCCCCAGCCTGTGGAAAGCCCCA
GCAGCTGAACCGGGTTGTGGCGGCCAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTGCTCACCAAGCCGCTGGGTGATC
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCATACTGTTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGAACCTGGCTCTGGTCCCAGAAGGTGGTGGCTGGTGGAGC
CCCACCCCTGTGTATTCCCTGGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGCCTGCCCATCTGCCTACCTGATGCCCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTTCCCTTGC
CCCACCCCTCAGACCCCTGCAGAAAGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGCTGTCTGGCGACTCCGGGGCCCCCTCATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCGGCATCATCAGCTGGGGCGAGGGCTGTGCCGAGCGAACAGGCC
GGGGTCTACATCAGCCTCTGCGCACCGCTCCTGGGTGGAGAAGATCGTGAAGGGTGCA
GCTCCGGGGCGCGCTCAGGGGGTGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGCCG
CCGCGCGCTCTAGGGCGCAGCGGACGCGGGCTCGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTGGCGGGCTCGGGCGTTCCCCCGCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCGGACGGCTGCTGCGAAAGGAAACCCCTCCCCGACCCGCCGAC
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCCGCCAACGGCCTCATGTCCCCGCCAAC
GACTTCCGGCCCCGCCGGGGCCCCAGCGCTTTGTGTATATAATGTTAATGATTTTAT
AGGTATTGTAACCTGCCACATATCTTATTATTCTCCAATTCAATAAATTATTATT
CTCCAAAAAA

FIGURE 98

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGCLGFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC
QVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSGQ
SGAAARS
```

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGGCCACCATGCACGGCTCTGCAGTTCTGATGCTTCTGCTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGCCCGTTGGAGCCCTCACAGATGAGGAGAACGTTGATGGT
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCTTCGCCAAGGCCCTACGCACGGCAGTGCCTGTGGGCCAC
AACAAAGGAGCGCGGGCGCCGCGAGAATCTGTTGCCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGCCAAGACAGAGAGGATC
GGCTGTGGTCCCACCTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGAACGTGAAGGGAAACGCCCTACCAGGAGGGACTC
CGTGCTCCCAATGTCCCTCTGGCTACCACGTCAAGAACTCCCTCTGTGAACCCATCGGAAGC
CCGGAAGATGCTCAGGATTGCCCTACCTGGTAACTGAGGCCCATCCTTCCGGCGACTGA
AGCATCAGACTCTAGGAAAATGGGTACTCCTTCCCTAGCAACGGGATTCCGGCTTCT
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCC
CCAACCTCCTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTGCGTAAC
AACTGAGGTCCCTCCATTGGCAGCTCACAGCCTGCCCTGGATGAGGAGCCAGTTA
CCTTCCCCAAATCGACCCATGTTCTATCCAAAATCAGCAGACAAAGTGAACAGACAAAACA
AAAGTGCCCTCTAGGAGCCCAGAGAACTCTCTGGACCCCCAAGATGTCCCTGACAGGGCAAG
GGAACTCCTACCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCTCCAGTG
AGGTCTTGGCCTCAGTTTCCAGGCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCCTCCAAGTCCCTGCCAATTCCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGCGTGCCTGGCTCTGCACTCGCTTGCAGGTGAGAGGGCCCTGACA
AGCCTAGCGTTGTCAAGGGCTGAACCTGGGCCCTGGTCACTGTGTGGGCCCTCTGGGA
CTACTGCTCCTGCCTCCTCTGGTGTGGCTGGAATCTCTGAATGGGATACCACCTAAAGGG
TGAAGAGGTAGCTGTCCTCCTGTCACTTCCCCACCCCTGTCCCCAGCCCCCTAAACAAGATA
CTTCTTGGTTAAGGCCCTCGGAAGGGAAAGGCTACGGGCATGTGCCTCATCACACCATCC
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCCTGAGGACTGCACACC
GGGCCACACCTCCTGCCCTCCCTCCTGAGTCCTGGGGTGGAGGATTGAGGGAGCT
CACTGCCTACCTGGCCTGGGCTGTCTGCCACACAGCATGTGCCTCTCCCTGAGTGCCTG
TGTAGCTGGGATGGGATTCCCTAGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGTTC
TTTGAGTGGGGAGGCAGGGACGAGGAAGGAAAGTAACCTGACTCTCCAATAAAACCT
GTCCAACCTGTGAAA

FIGURE 100

MHGSCSFLMLLPLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDMLHMRWDEE
LAAFAKAYARQCVWGHNKERRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQC
PSGYHCKNSLCEPIGSPEDAQDLPYLVTEAPSFRATEASDSRKMGTPLLATGIPAFLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAHSPLSLDEEPVTFPKS
THVPIPKSADKVTDKVPSRSPENSMDPKMSLTGARELLPHAQEEAEAEELPPSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV
SGLNSGPVHVGPLLGLLLLPLVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAACGTGAAAGTCAGGCTTTCATTGGGAAGCCCCCTCAACAGAACCGTCAATTCTCCAAGTTATGGTGGACGT
ACTTCTGTTGTTCTCCCTCTGCTTGCCTTACATTAGCAGACCGGACTTAAGTCACAACAGATTATCTTTCAT
CAAGGCAAGTTCCATGAGCCACCTTCAAAGCCTCGAGAAGTGAACAAACAAATGAATTGGAGACCAATTCC
AAATCTGGGACCAGTCTGCCAAATATTACACTCTCTCCCTGGCTGAAACAGGATTGTTGAAACTCTCCCTGA
ACATCTGAAAGAGTTCAGTCCCTGAAACTTTGGACCTTAGCAGCAACAATATTTCAGAGCTCCAAACTGCATT
TCCAGCCCTACAGCTAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTGACAA
TTTGGCCAACACACTCCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTAAACT
GCCCAACTGCAACATCTGAATTGAACCGAAACAAGATTAAGATGAGATGGACTGACATTCCAAGGCCTTGG
TGCTCTGAAAGTCTCTGAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTGGGGCTGAGCAA
CATGGAAACTTTCATCTCAGCCAAATGCCCACAGGATCAGCCCTGATGCCCTGGAGTTCTGCCAGAAGCTCAG
GCAGGACTGACCTAACTTCAATCAAGGTTAGATGATTCAAGCTTCCCTGGCCTAAGCTTAACTAAAC
ACTGCACATTGGGAAACACAGTCAGCTACATTGCTGATTGTGCTTCCGGGGCTTCCAGTTAAAGACTTT
GGATCTGAAGAACATGAAATTCTGGACTATTGAAGACATGAATGGTCTTCTGGGTTGACAAACTGAG
GCGACTGTAACTCCAAGGAATCGGATCCGTTCTATTACTAAAAAGCCTTCAGGGTTGGATGCATTGGAGCA
TCTAGACCTGAGTGACAACGCAATCATGTCTTACAAGGCAATGCATTTCACAAATGAAGAAACTGCAACAAATT
GCATTAAATACATCAAGCCTTTGTGCGATTGCCAGCTAAATGGCTCCACAGTGGGTGGCGAAACAAACTT
TCAGAGCTTGTAAATGCCAGTTGTGCCCCATCTCAGCTGCTAAAGGAAGAACGATTTTGTGTTAGCCCAGA
TGGCTTGTGTTGATGATTTCCAAACCCCAGATCACGGTTCAGCCAGAAACACAGTCGCAATAAAAGGTT
CAATTGAGTTTCATCTGCTCAGCTGCCAGCAGCAGTGATTCCCAATGACTTTGCTTGGAAAAAAAGACAATGA
ACTACTGCATGATGCTGAAATGGAAATTATGCACACCTCCGGGCCAAGGTGGAGGTGATGGAGTATACCAC
CATCCTTCGGCTGCGCAGGTGGAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCCAATCACTTTGGTT
ATCCTACTCTGCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTCACCAAGACCCCCATGGATCTCACC
CCGAGCTGGGGCCATGGCACGCTTGGAGTGCTGCTGTGGGCACCAGCCCCCAGATAGCCTGGCAGAAGGA
TGGGGGACAGACTTCCAGCTGCACGGAGAGACGCATGATGTGATGCCAGGGATGACGTGTTCTTATCGT
GGATGTGAAGATAGAGGACATTGGGTATAACAGCTGCACAGCTCAGAACACAGTGCAAGGAGTATTTCAGCA
AACTCTGACTGCTCTAGAACACCATATTTCGCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGC
CGTCCTACAGTGCATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTGGG
AACCGAGAGGCATTTCAGCAGGCAATCAGCTCTGATTATTGTTGACTCAGATGTGATGCTGGGAA
ATACACATGTGAGATGCTAACACCCCTGGCACTGAGAGAGAACGTGCGCCTCAGTGTGATCCCCACTCCA
CTGCGACTCCCCCTCAGATGACAGCCCCATCGTAGACGATGGCAGTGGGTGTCATCATACACACAAAGGG
CGTGGTTGCTGTGGCAGTCACTCGTGTGGGTGTCATCATACACACAAAGGGGAGGAATGAAGA
TTGCAAGCATTACCAACACAGATGAGACCAACTTGCAGCAGATATTCTAGTTATTGTCATCTCAGGG
AGCTGACAGGCAGGATGGGTACGTGCTTCAGAAAGTGGAGGCCACCCAGTTGTCACATCTCAGGTGCTGG
ATTTTCTTACACACATGACAGTAGTGGGACCTGCCATTGACAATAGCAGTGAAGCTGATGTGGAGCTGC
CACAGATCTGTTCTTGTCCGTTTGGGATCCACAGGCCCTATGTATTGAAGGGAAATGTGATGGCTCAGA
TCCTTTGAAACATATCATACAGGTTGCACTGCCAGCCAAAGAACAGTTTAATGGACCAACTGAGGCCAGTT
CATAAAGAAAAGGAGTGTACCCATGTTCTCATCCTCAGAAGAACCTGCGAACGGAGCTCAGTAATATAC
GTGGCCTTCACATGTGAGGAAGCTACTTAACACTAGTTACTCTCACAATGAAGGGACCTGGATGAAAATCTGT
TCTAAACAAGTCTCTTGTGAAATCCAGAGGCCAGCGTCGGTGCCTCGAGTAATTCTTCTATGGG
TACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGCCATCAGATTGT
AAGAGCCTTTATTGAAAGCTCATTCTCCCCAGACTTGGACTCTGGGTGAGGAAAGATGGGAAAGAAAGGAC
AGATTTCAAGGAAGAAAATCACATTGTAACCTTAAACAGACTTGTAGAAAACAGACTCCAAATTTCAGTC
TTATGACTTGGACACATAGACTGAATGAGACCAAGGAAAAGCTTAACATACTACCTCAAGTGAACTTTATT
AAAGAGAGAGAATCTTATGTTTAAATGGAGTTATGAATTAAAAGGATAAAATGCTTTATTATACAGAT
GAACCAAAATTACAAAAGTTATGAAAATTCTACTGGGAATGATGCTCATATAAGAACCTTTAAACTA
TTTTTAACCTTGTGTTATGCAAAAAAGTATCTACGTAATTAAATGATATAAAATCATGATTATTTATGTATT
TTATAATGCCAGATTCTTTATGAAAATGAGTTACTAAGCATTAAATAACCTGCCATTGACCACTTT
TTAAATAGAAGTTACTTCATTATATTGACATTATATTAAATAAAATGTGCAATTGAA

FIGURE 102

MVDVLLLFSLCLLFHISRPDLSHNRLSFIAKASSMSHLQSLREVKLNNELETIPNLGPVSAN
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP
GYFDNLANTLLVLKLNRRNRIASIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKM
QRNGVTKLMGDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPAWE
FCQKLSELDLTFNHLRSRLLDDSSFLGLSLLNLTIGHNNRVSYIADCAFRLSSLKTLIDLKNNE
ISWTIEDMNGAFSGLDKLRRLLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQ
MKKLQQLHLNTSSLLCDCQLKWLPOWVAENNFSFVNASCAPOLLKGRSIFAVSPDGFVCD
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKDNELLHDAEMENYAHLRAQG
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYVKAKLTVNMLPSFTKTPMDLTIRAGA
MARLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN
SAGSISANATLTVLETPSFLRPLLDRVTKGETAVLQCIAGGSPPPKNWTKDDSPLVTER
HFFAAGNQLLIVDSDVSDAGKYTCMSNTLGTTERGNVRLSVIPTPTCDSPQMTAPSLODDG
WATVGVIIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNLPADIPSYLLSSQGTTLAD
RQDGYSSESSESHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGP
MYLKGNVYGSDPFETYHTGCPDPRTVLMHYEPSYIKKKECYPCHPSEESCRSFNISW
PSHVRKLLNTSYSHNEPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA
YSSFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGAAAAGGAGACTTTTTGGTGGTGGCTGTTGGGTGCCTTGCAAAAATG
AAGGATGCAGGACGCAGCTTCTCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAACGAAAC
GAAGCTTTCTGTGAGCCCTGGATCTAACACAAATGTGTATATGTGACACACAGGGAGCATTCAAGAATGAAA
TAAACCAGAGTTAGACCCGGGGGTGGTGTCTGACATAAATAATCTTAAAGCAGCTGTTCCCCTCC
CCACCCCCAAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTCAACAAAGAAAAAGTATGTTCAATTTC
TATAAAGGAGAAAGTGGAGGAGATTTTGGAAATGAAAAGTTGGGGCTTTTAGTAAAGTAAAGAAGACT
GGTGTGGTGGTCTTCTTGTGAAATTCCCACAGGAGAGGAAATTAAATAACATCTGCAAAGAAA
TTTCAGAGAAGAAAAGTTGACCGCGGAGATTGAGGCATTGATTGGGGAGAGAACAGCAGAGCACAGTTGGA
TTTGTGCTATGTTGACTAAAATTGACGGATAATTGCACTGGATTTTCTTCATCAACCTCTTTTTAAAT
TTTATTCTTTGGTATCAAGATCATGCGTTCTCTGGTCTTAACACCTGGATTTCATCTGGATGTTGCT
GTGATCAGTCTGAAATACAATGTTGAATTCCAGAACAGGACAAACACAGATAAAATTATGAATGTTGAAAGAT
GACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTAACAGGGCCATTGACCCCTGCTTGTTGCT
GCTGGCTTCACTTCTGGTGGCTGGTCTGGCTAGACCTGCCCTCTGTGCTCCTGCAGCAA
CCAGTTCAAGGTGATTGTGTTGGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCCACCAACACAGGCT
GCTGAACCTCCATGAGAACCAATCCAGATCATCAAAGTGAACAGCTCAAGCAGTGAGGACTTGGAAATCCT
ACAGTTGAGTAGGAACCATATCAGAACATTGAAATTGGGGCTTCAATGGTCTGGCAACCTCAACACTCTGGA
ACTCTTGACAATCGTCTTACTACCATCCGAATGGAGCTTTGTATACTTGTCTAAACTGAAGGAGCTGGTT
GCGAAACAACCCATTGAAAGCATCCCTTCTATGCTTTAACAGAAATTCTTCTTGCGCCGACTAGACTTAGG
GGAATTGAAAAGACTTTCATACATCTCAGAAGGTGCTTGAAGGTCTGCTAACATTGAGGATTGAAACCTTG
CATGTGCAACCTCGGGAAATCCCTAACCTCACACCGCTCATAAAACATAGATGAGCTGGATCTTCTGGAAATCA
TTTATCTGCCATCAGGCCTGGCTCTTCCAGGGTTGATGCACCTTCAAAACTGTGGATGATACTGCCCAGAT
TCAAGTGATTGAAACGGAATGCCCTTGAACACCTCAGTCAGTGGAGATCAACCTGGCACACAATAATCTAAC
ATTACTGCCTCATGACCTCTCACTCCCTTGACATCTAGAGCGGATACATTACATCACAAACCTTGGAACTG
TAACCTGTGACATACTGTGGCTCAGCTGGGATAAAAGACATGGCCCTCGAACACAGCTTGTGCCCCGGTG
TAACACTCCCAACTTAAAGGGGGGTACATGGAGAGCTGACCGAGAATTACTTCACATGCTATGCTCCGGT
GATTGTGGAGCCCCCTGCAACCTCAATGTCAGTGAAGGCATGGCAGCTGAGCTGAAATGTGGGCTCCACATC
CCTGACATCTGTATCTGGATTACTCCAATGGAACAGTCATGACACATGGGGCTACAAAGTGGGATAGCTGT
GCTCAGTGTGGTACGTTAAATTTCACAAATGTAACACTGTGCAAGATAAGGAGTACAGGAGTACATGTTGAGTAA
TTCCGGTGGGAAACTACTGTGCTCAGCCACCTGAATGTTACTGCAAGCAACCAACTACTCTTCTTTACTTTTC
AACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGGACCACAGATAACAATGTGGTCCCACCTC
AGTGGTCAGTGGAGACCAATGTGACCACTCTCACACCAACAGAGCACAGGTCGACAGAGAAAACCTT
CACCATCCCAGTGAATGATATAAACAGTGGGATCCCAGGAATTGATGAGGTATGAAGACTACAAAATCATCAT
TGGGTGTTTGTGGCCATCACACTCATGGCTGAGTGTGCTGGTCTTCTACAAGATGAGGAAGCAGCACCA
TCGGCAAACCATCACGCCCAACAAGGACTGTTGAAATTATTAATGTGGATGAGATTACGGGAGACACACC
CATGGAAAGCCACCTGCCATGCCTGCTATCGAGCATGAGCACCTAAACTATAACTCATACAAATCTCCCT
CAACCAACAAACAGTTAACACAATAATTCAATACACAGTCAGTCATGAACCGTTATTGATCCGAATGAA
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACACATTACAGAGTTACAAAAACAAACATCAAAAAAA
GACAGTTTATTAAAAATGACACAAATGACTGGCTAAATCTACTGTCTTTACAAAAAGTGTCTTACAAAAAA
AAAAGAAAAGAAATTATTATTAAAAATTCTATTGTGATCTAAAGCAGACAAAAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLVVLLALQLLVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGISTNTRLLNLHENQIQIIVKNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPLRRLLGELKRLS
YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLPHDLFTPPLHHLERIHLHHNPWNCNCIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNTEGMAAE
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTQDTGMYTCMVSNSVGN
TTASATLNVTAAATTTFPSYFSTVTVETMEPSQDEARTDDNNVGPTPVVDWETTNVTTSLTPQ
STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIIINVDEITGDTPMESHLPMPAIEHEHLNHYNSYKSPFNHTTVNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTCAGTTGGCAGTTCTGGTTCCCTGCTGTTGGGGCA
TGAAAGGGCTTCGGCGCCGGAGTAAAAGAAGAATTGACCGGGCAGCGCGAGGGAGGAGCGCGCACCGCACCGC
GAGGGCGGGCGTGCACCCCTCGGCTGGAAGTTGTGCCGGCCCCGAGCGCGCCGGCTGGAGCTTCGGGTAGA
GACCTAGGCCGCTGGACCGCG**ATG**AGCGCGCCAGCCTCCGTGCGCGCCGGGGTTGGGCTGCTGCTGTGC
GCGGTGCTGGGGCGCGCTGGCGCTCCGACAGCGGGCTCCGGGGAACTCGGCAGCCCTCTGGGGTAGCGGCC
GAGCGCCCATGCCCACTACCTGCCGCTGCCCTGGGACCTGCTGGACTGCAAGCGCTAGCGCGTCTT
CCCGAGCCACTCCGCTGGCTGGACTTAAGTCACAACAGATTATCTTCATCAAGGCAAGTCC
ATGAGCCACCTCAAAGCCTCGAGAAGTAACTGAACAACAATGAATTGGAGACCATTCAAATCTGGGACCA
GTCTGGCAAATATTACACTCTCTGGCTGGAAACAGGATTGTAAGAAACTCCCTGAAACATCTGAAAGAG
TTTCAGTCCTTGAAACTTTGGACCTTAGCAGCAACAATTTCAGAGCTCAAACGTGCAATTCCAGCCCTACAG
CTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTGACAATTGGCAACACA
CTCCCTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAAGATGTTAAACTGCCCAACTGCAA
CATCTCGAATTGAAACGAAACAAGATTAAAATGTAGATGGACTGACATTCAAGGCCCTGGCTCTGAAAGTCT
CTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTGGGGCTGAGCAACATGGAATTGG
CAGCTGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTACGGCTGATGCTGCAGGAACCTCAT
CTCAGCCAAATGCCATCAACAGGATCAGCCCTGATGCCCTGGAGTCTGCCAGAAGCTCAGTGAGCTGGACCTA
ACTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCTGGCTTAAGCTTAAACTACATGCACATTGGG
AACAAACAGAGTCAGTACATTGCTGATTGTGCCCTCCGGGGCTTCCAGTTAAAGACTTGGATCTGAGAAC
AATGAAATTTCCTGGACTATTGAAGACATGAATGGTCTTCTGGCTTGACAAACTGAGGCGACTGATACTC
CAAGGAAATCGGATCCGTTCTATTACTAAAAAACGCTTCACTGGTTGGATGCAATTGGAGCATCTAGACCTGAGT
GACAACGCAATCATGCTTTACAAGGCAATGCAATTTCACAATGAAGAAACTGCAACAATGCAATTAAATACA
TCAAGCCTTTTGCGATTGCCAGCTAAATGGCTTCCACAGTGGTGGCCAAAACAACTTCAAGAGCTTGT
AATGCCAGTTGTGCCATTCTCAGCTGCTAAAGGAGAACGATTTTGCTGTTAGCCAGATGGCTTGTGTT
GATGATTTCCAAACCCCAGATCACGGTTAGCCAGAAACAGTCCGCAATAAAAGGTTCAATTGAGTTTC
ATCTGCTCAGCTGCCAGCAGCAGTGTACCCCCATGACTTTGCTGGAAAAAAAGACAATGAACACTGCA
GCTGAAATGGAAAATTATGACACCTCCGGGCCAAGGTGGCAGGGATGGAGTACCAACATCCTTCGGCTG
CGCAGGGTGAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCAATTCACTTGGTTCATCCTACTCTGTC
AAAGCCAAGCTACAGTAAATATGCTTCCCTCATCAGGAAACAGCAGGCTTGGCTGGCCACAGC
ATGGCACGCTGGAGTGTGCTGCTGGGGCACCCAGCCCCCCAGATAGCCTGCCAGAAGGATGGGGCACAGAC
TTCCAGCTGCACGGAGAGACGCATGCATGTGATGCCAGGGATGACGTGTTCTTATGTGGATGTAAGATA
GAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTCAGCAAATGCAACTCTGACTGTC
CTAGAAACACCATCATTGGCGCCACTGTTGGACCGAATGTAACCAAGGGAGAAACAGCCGCTTACAGTGC
ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACGGACAAAGATGATAGCCATTGGTGTAAACGAGAGGCAC
TTTTTGCAAGCAGGCAATCAGCTCTGATTATTGTGGACTCAGATGTCAGTGCTGGAAATACACATGTGAG
ATGCTAACACCCCTGGCACTGAGAGAGGAAACGTCAGTGATCCCAACTCCAACTGCGACTCCCCCT
CAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCACTGTTGGGTGTCGTGATCATAGCCGTTGCTGT
GTGGGGCACCTACTCGTGTGGGTCATCATATAACACACAAGGGGAGGAATGAAGATTGCAAGCATTAC
AACACAGATGAGACCAACTTGCAGAGATATTCTCATCTCAGGGAAACGTTAGCTGACAGGCAG
GATGGGTACGTGCTTCAAGAAAGTGAAGGCCACCCAGTTGTCACATCTCAGGTGCTGATTCTTACCA
CAACATGACAGTAGTGGACCTGCCATTGACAATAGCAGTGAAGCTGATGTAAGCTGCCACAGATCTGTT
CTTTGTCGTTTTGGGATCCACAGGCCCTATGTATTGAAAGGGAAATGTGTATGGCTCAGATCCTTTGAAACA
TATCATACAGGTTGCAGTCTGACCCAGAACAGTTAAATGGACCAATGAGCCAGTTACATAAAAGAAAAAG
GAGTGCACGGCTACCCATGTTCTCATCTCAGAAGAACCTGCAGGGAGCTTCAAGTAAATATCTG
GTGAGGAAGCTACTAACACTAGTTACTCTCACAAATGAAGGACCTGGAAATGAAAATCTGTTCTAAACAAGTCC
TCTTGTGTTTTAGTGCAGGAACTCCAGAGCCAGCGTCGGTCTCGAGTAATTCTTCATGGTACCTTTGGAAA
GCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGCCATCAGATGTCAGGCCAGAGCCTTTAT
TTGAAAGCTATTCTCCCCAGACTTGGACTCTGGGTCAAGAGGAAGATGGAAAGAAAGGACAGATTTCAGGAA
GAAAATCACATTGTACCTTAAACAGACTTAAAGGGAAACTACAGGACTCCAAATTTCAGTCTTATGACTTGGAC
ACAT**AG**ACTGAATGAGACCAAAGGAAAGCTTAACATACTACCTCAAGTGAACCTTATTAAAGAGAGGAAT
CTTATGTTTTAAATGGAGTTATGAATTAAAGGATAAAATGCTTTATTATACAGATGAACCCAAATTAC
AAAAAGTTATGAAATTAACTGGGAATGATGCTCATATAAGAAACCTTTAAACTATTAACTTTAACTTTG
TTTTATGAAAAAGTATCTACGTAATTAAATGATATAATCATGATTATTATGTATTAAATGCCAGA
TTCTTTTATGGAAATGAGTTACTAAAGCATTAAATAACCTGCCCTGTACCATTTTAAATAGAAGTT
ACTTCATTATATTGCACTTAAATGTCATTAAATGTCATTGAAAAA

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCPTTCRCLGDLDDCSR
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNELETIPNLGPVSANIT
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY
FDNLANTLLVLKLNRRNRIASIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKMQR
NGVTKLMGDGFGLSNEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWEFC
QKLSELDLTFNHLSDLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLSSLKTLDLKNNEIS
WTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK
KLQLQHLNTSSLLCDCQLKWLPOQWAENFQSFVNASCAPQLLKGRSIFAVSPDGVCDDF
PKPQITVQPETQSAIKGSNLNFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRAQGGE
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVAKLTNVNMLPSFTKTPMDLTIRAGAMA
RLECAAVGHPAPQIAWQKDGGETDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA
GSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKNWTKDDSPLVVTERHF
FAAGNQLLIIVDSDVSDAGKYTCEMSNTLTERGNVRLSVIPTPTCDSPQMTAPSLLDDGWA
TVGVVIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNLPADIPSYLSSQGTLADRO
DGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY
LKGNVYGSDFETYHTGCPDPRTVLMHYEPSYIKKKECYPCHSEESCRSFSNISWPS
HVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDAYS
SFGQPSDCQPRAFYLKAHSSPDLGSEEDGKERTDFQEENHICTFKQTLNEYRTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519, 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378, 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735, 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022, 1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433, 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

CAAAACTTGCCTCGCGAGAGCGCCCAGCTTGAATGGAAGGAGCCCAGGCCGGAGCGCAGCTGAGAC
TGGGGGAGCGCGTTCGGCCTGTGGGCGCCGCTCGCGCCGGGCGCAGCAGGGAAAGGGGAAGCTGTGGCTGCC
CTGCTCCACGAGGCAGCCACTGGTGTGAACCGGGAGAGGCCCTGGGTGGTCCCGCCCTATCCCTCTTTATATA
GAAACCTTCCACACTGGGAAGGCAGGCCGGAGGGCAGGGCTCATGGTGAAGCAAGGAGGCCGGCTGATCTGCAG
GCCAGCAGCATTCCGAGTTACAGATTTACAGATAACCAATGGAAGGCAGGGCAGAACAGCCTGCCTGGT
TCCATCAGCCCTGGCAGGCAGCGCATCTGACTCGGCACCCCTGCAGGCACCATGGCCAGGCCGGGTGCTGC
TGCTCCTGCTGCTGCCACAGCTGCACCTGGGACCTGTGCTTGCCTGAGGGGCCAGGATTTGGCCGAA
GTGGCGCCACAGCCTGAGCCCCGAAGAGAACGAATTGCGGAGGAGGAGGCCGGTGTGGTACTGAGCCCTGAGG
AGCCCCGGCCTGGCCAGCCGGTCAAGCTGCCCTGGAGACTGTGCTTGCCTGAGGGGCTGCTGAGCTGTG
GCGGTATTGACCTGCGTGAAGTCCCGGGGACCTGCTGAGCACACCAACCACCTATCTCTGAGAACAAACCAGC
TGGAAAAGATCTACCCCTGAGGAGCTCTCCGGCTGCACCGCTGGAGACACTGAAACCTGAAACAAACCGCCTGA
CTTCCCAGGGCTCCAGAGAAGGCTTGAACATCTGACCAACCTCAATTACCTGACTTGGCAATAACAAGC
TGACCTTGGCACCCGCTTCTGCCAACGCCCCGATCAGTGTGGACTTGTGCTGCCACTATCTACCAAGATCT
ATGGGCTCACCTTGGCCAAGGCAAACCTTGAGGTCTGTGTACCTGACAACAACAAGCTGGCAGACGCCGGC
TGCCCGACAACATGTTCAACGGCTCCAGCAACGTCAGGCTCTCATCTGTCCAGCAACTTCTGCGCCACGTGC
CCAAGCACCTGCCCTGCCCTGTACAAGCTGCACCTCAAGAACACAAGCTGGAGAAGATCCCCCGGGGCT
TCAGCGAGCTGAGCAGCCTGCGAGCTATAACCTGAGAACAAACTACCTGACTGACGGGGCTGGACAACGAGA
CCTTCTGGAAGCTCTCAGCCTGGAGTACCTGGATCTGTCCAGCAACAACCTGTCAGGGTCCCAGCTGGCTGC
CGCGCAGCCTGGTGTGCTGCACTTGGAGAAGAACGCCATCCGGAGCGTGGACGGAATGTGCTGACCCCCATCC
GCAGCCTGGAGTACCTGCTGCTGCACAGCAACCAGCTGCCGGAGCAGGGCATCCACCCACTGGCCTTCCAGGGCC
TCAAGCGGTTGACACGGTGCACCTGTACAACAACGCGCTGGAGCGCGTGCCTAGTGGCTGCTGCGCTG
GCACCCCTCATGATCCTGACAACCAGATCACAGCATTGGCGGAAGACTTTGCCACCACCTACTTCTGGAGG
AGCTCAACCTCAGCTACAACCGCATCACCAGGCCACAGGTGCAACCGCGACGCCCTCGCAAGCTGCGCTGCTGC
GCTCGCTGGACCTGTGGCAACCGGCTGCACAGCTGCCACCTGGCTGCCTCGAAATGTCCATGTGCTGAAGG
TCAAGCGCAATGAGCTGGCTGCTGGCAAGGGGGCTGGCGCATGGCTCAGTGTGGAGCTGTACCTCA
CCAGCAACCGACTGGCAGCCGAGCCCCCTGGGCCCCCTGCTGGGTGACCTCGCCCATCTGCAGCTGCTGGACA
TCGCCGGGAATCAGCTCACAGAGATCCCCGAGGGCTCCCGAGTCAGTGTGACTTGTGAGAACACAACA
AGATTAGTGCCTGGTGCCTGCAACTCCACGCCAACCTCAAGGGGATCTTCTCAGGTTAACAAAGC
TGGCTGTGGGCTCCGTGGTGGACAGTGCCTTCCGGAGGCTGAAGGACCTGCAAGGTCTGGACATTGAAGGCAACT
TAGAGTTGGTGAACATTCCAAGGACCGTGGCCCTTGGGAAGGAAAGGAGGAGGAGGAAGGAGGAGGAGGAGG
AGGAAGAGGAAACAAGATAGTGACAAGGTGATGCAAGATGTGACCTAGGATGATGGACCGGGACTCTTTCTGC
AGCACACGCTGTGCTGAGCCCCCACTGCGCTGCACACAGACACACCCAGCTGCACACATGAGGCA
TCCCACATGACACGGGCTGACACAGTCTCATATCCCCACCCCTCCACGGCGTGTCCCACGGCCAGACACATGC
ACACACATCACACCCCTCAAACACCCAGCTCAGCCACACAACTACCCCTCAAACCAACACCACAGTCTGTGACAC
CCCCACTACCGCTGCCACGCCCTCTGAATCATGCAGGGAAGGGCTGCCCTGCCACACACAGGCCACCA
TTCCCTCCCCCTGCTGACATGTGATGCTGATGCAACACACACACATGCACAAGTCATGTGCGAA
CAGCCCTCAAAGCTATGCCACAGACAGCTTGCCTGCCAGCCAGAATCAGCCATAGCAGCTGCCGTGCCCT
GTCCATCTGCTCCGTCCGTTCCCTGGAGAAGACACAAGGTATCCATGCTGTGGCCAGGTGCCCTGCCACCCCTCT
GGAACCTACAAAAGCTGGCTTTATTCCCTTCCATCCTATGGGACAGGAGCCTCAGGACTGCTGGCCTGGCC
TGGCCACCCCTGCTCCTCCAGGTGCTGGCAGTCACTCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA
CAGGCAGCTTCCAAATGGGCAAGGCCAGTGGAGGCAGGATGGGAGAGGCCCTGGGTGCTGCTGGGCTTGGGG
CAGGAGTGAAGCAGAGGTGATGGGCTGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGAACCTTT
GTTCTCAGGCCCTGTGGGGGAAGTTCCGGGTGCCCTTATTCTTTCTAAGGAAAAAAATGATAAAAAT
CTCAAAGCTGATTTCTTGTATAGAAAAACTAATATAAAAGCATTATCCCTATCCCTGCAAAAAAA

FIGURE 108

MEGEEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPPEENEFAEEEVLVLSPEEPGPGPAAVSCPRDCACSQEGVVDCGGIDLREFPGDLP
EHTNHLQLQNNQLEKIYPEELSRLHRLETLNLQNNRLTSRGLPEKAFFEHTNLNYLYLANNK
LTLPAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV
EVLISSNFLRHVPKHLPPALYKLHLKNNKLEKIYPPGAFSELSSLRELYLQNNYLTDEGLDN
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSDANVLTPIRSLEYLLLHSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPDRVRTLMILHNQITGIGREDFATTYF
LEELNLSYNRITSPOVHRDAFRKLRLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNELAALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDASFRRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341, 477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGGAGGGGGCTCCGGGCGCCGCAAGCAGACCTGCTCCGGCCGCGCCCTGCCCGCTGTCTCCGGGAGCGGCAG
CAGTAGCCCGGGCGGGAGGGCTGGGGTTCTCGAGACTCTCAGAGGGCGCTCCCATCGCGCCCACCA
CAACCTGTCCTCGCGGCCACTGCGCTGCCAGGACCCAGCTGCCAACATGGATTCTCTGGCGCTGGT
GCTGGTATCCTCGCTACCTGCAGGGGCCGAGTTGACGGGAGGTGGCCAGGCAAATAGTGTATCGAT
TGGCCTATGCTTATGGTGGGAGGATTGACTGCTGCTGGGCTGGCCAGTCTGGGGACAGTGTAGCC
TGTGTGCCAACACAGTCAAACATGGTGAATGTATCGGCCAACAAAGTCAAGTGTATCTGGTTATGCTGG
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCCTGAAGCCCCGGCCCTGTAAGCAGGTGATGAAACACTTA
CGGCAGCTACAAGTCTACTGCTCAAGGATATATGCTCATGCCGGATGGTCTGCTCAAGTGCCCTGACCTG
CTCCATGGCAAACGTCAAGTATGGCTGTGATGTTAAAGGACAAATACGGTGCCAGTGCCATCCCTGGCCT
GCACCTGGCTCCTGATGGGAGGACCTGTTGATGAAATGTGCTACAGGAAGAGCCTCTGCCCTAGATT
TAGGCAATGTGTCACACTTTGGGAGCTACATCTGCAAGTGTATGCAAAAGGCTTCGATCTCATGTATATTGGAGG
CAAATATCAATGTATGACATAGACCAATGCTACTTGGTCAGTATCAGTGCAGCAGCTTGCTCGATGTTAA
CGTACGTGGGCTCTACAAGTCAAATGTAAGAAGGATACCAAGGGTGTGGACTGACTGTTGTTGATATCCCAA
AGTTATGATTGAAACCTTCAGGTCCTGAAATTGATGACAAAGGGAAATGGTACCATTTAAAGGGTACACAGGAA
TAATAATTGGATTCTGATGTTGGAGTACTTGGTGGCCTCGAAGACACCATATATTCCCTCTATCATTACCAA
CAGGCCTACTCTAAGCCAACAAGACCTACACCAAGCCAACACCAATTCTACTCCACCACCACC
CCTGCCAACAGAGCTCAGAACACCTTACCCACCTACAACCCAGAAAGGCCAACACCAGACTGACAACATAGC
ACCAGCTGCCAGTACACCTCCAGGAGGGATTACAGTTGACAACAGGGTACAGACAGACCCCTCAGAAACCCAGAGG
AGATGTGTTAGTGTCTGGTACACAGTTGTAATTGACCATGGACTTGTGGATGGATCAGGGAGAAAGACAA
TGACTTGCACTGGGAAACCATCAGGGACCCAGCAGGTGGACAATATCTGACAGTGTGGCAGCCAAAGCCCCAGG
GGGAAAAGCTGCACGCTGGTGTACCTCTGGCCGCTCATGCATTAGGGGACCTGTGCTGTCAATTGAGC
CAAGGTGACGGGGCTGCACTCTGGCACACTCCAGGTGTTGTGAGAAAACACGGTGGCCACGGAGCAGCCCTGTG
GGGAAGAAAATGGTGGCCATGGCTGGAGGCAAACACAGATCACCTTGCGAGGGGGTGTGACATCAAGAGCGAATCACA
AAAGATGATTAAGGGTTGGAAAAAAAGATCTATGATGGAAAATTAAGGAACCTGGGATTATTGAGCCTGGAGAAAG
AGAAGACTGAGGGCAAACATTGATGGTTCAACTGATGGTTTCAAGTATATGAAGGGTTGGCACAGAGGGTGGCACCAGCTG
TTCTCCATATGCACTAAGAACAGAGGAAACTGGCTTAGACTAGAGTATAAGGGAGCATTCTGGCAGG
GGCCATTGTTAGAATACTTCATTAAGATGGTAAAGATGTTTACCCAAGGAAAAGTAAACAAATTATAGAATTCCCAA
AGATGTTTGATCCTACTAGTAGTATGCACTGAAAGGGGATTGAAAGGGGAAGAGCCCACAAATGCTGAGCTCACTGAAATA
TCTCTCCCTATGGCAATCTAGCAGTATTAAGAAAAAGGAAACTATTATCCAAATGAGAGTATGATGGAC
AGATATTGTTAGTATCTCAGTAATGTCTAGTGTGGCGGTGTTCAATGTTCTCATGGTAAAGGTATAAGCC
TTTCATTGTTCAATGGATGATGTTCAAGATTTTTTTAAGAGATCCTCAAGGAACACAGTTAGAGAG
ATTTTCATGGGTGCATTCTCTGCTCGTGTGACAAGTTCTGGCTGCTGAGAAAGAGTGCCCTGCC
ACACCGGCAGACCTTCCTCACCTCATCAGTATGATTCAAGTGTCTCTTATCAATTGGACTCTCCAGGTCCAC
AGAACAGTAATATTTTGAAACAATAGGTACAATAGAAGGTCTCTGTCAATTAAACCTGGTAAAGGCAGGGCTGG
AGGGGGAAAATAATCATTAAGCCTTGAGTAACGGCAGAATATATGGCTGTAGATCCATTGTTAATGTT
TCCTTTATGGTCAATATAACTGCACTGAAAGATGAAAGGGAAAATAATGAAATTGTTACTTTGATGCCAA
TGATACATTGCACTAAACTGATGAAAGAAGTTATCCAAAGTACTGTATAACATCTGTTATTATTAATGTTT
CTAAAATAAAAATGTTAGTGGTTTCCAATGGCCTAATAAAAACAATTATGAAATAAAACACTGTTAGTAAT

FIGURE 110

MDFILLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCOPVCQP
RCKHGE CIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGCDVVKGQIRCQCPSPGLHLAPDGRTCVDVDECATGRASCPFRQC
VNTFGSYICKCHKGFDLMLYIGGKYQCHDIDECSLGQYQCSSFARCYNRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKGNGTILKGDTGNNNWIPDVGSTWWPPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPPLPTELRTPLPPTTPERPTTGLTTIAPA A STPPGGITVDN
RVQTDPQKPRGDVF SVL VHS CNFDHGLCGWI REKDNDLHWEPI RD PAGGQYLT VSAAKA PGG
KAARLVLPLGRLMHSGDLCLSFRHKVTGLHS GTLQVFVRKHGAHGAALWGRNGGHGWRQTQI
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTTGCCCTTAGATTGTGA
AATGTGGCTCAAGGTCTCACAACTTCCCTTGCAACAGGTGCTGCTCGGGGCTGA
AGGTGACAGTGCCATCACACACTGTCATGGCGTCAGAGGTAGGCCCTACCTACCGTC
CACTATGGCTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGAGAGACCCCA
ACAATGCCAAATACTTACTGGCTCTGTGAATAAGTCTGTGGTCTGACTTGGAAATACC
AACACAAGTCACCATGATGCCACCAATGCATCTGCTTATCAACCCACTGCAGTTCCCT
GATGAAGGCAATTACATCGTGAAGGTCAACATTCAAGGAAATGGAACACTATCTGCCAGTCA
GAAGATAACAAGTCACGGTTGATGATCCTGTACAAAGCCAGTGGTGCAGATTCATCCTCCCT
CTGGGGCTGTGGAGTATGTGGGAACATGACCTGACATGCCATGTGGAGGGGGACTCGG
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC
TCCCCAAAACAATACCCCTCATATTGCTCCAGTAACCAAGGAAGACATTGGAAATTACAGCT
GCCTGGTGAGGAACCTGTCAGTGAAATGGAAAGTGATATCATTATGCCCATCATATATTAT
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTACTGT
TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAATACTACATATCATTAAGCATGGCCTCGCTAGAAGTT
GCATCTGAGAAAGTAGCCCAGAAAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAAC
CGGCAGGCAAGATGAAACTCATTACAGTTACATCACCTCCGTAGGACTGGAGAAGCTTG
CACAGAAAGGAAAATCATTGTCACCTTAGCAAGTATAACTGGAATATCACTATTTGATT
ATATCCATGTGTCCTCTCTTCTATGGAAAAAAATATCAACCCATCAAAGTTATAAAACAGAA
ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAGCTCAAACATTTCAGGCCATGAAGATG
CTCTGGATGACTCGGAATATATGAATTGTTGCTTTCCAGATGTTCTGGTGTTCAGG
ATTCCAAGCAGGTCTGTCAGCCTCTGATTGTGTATCGGGCAAGATTGCACAGTACAGT
GTATGAAGTTATTCACTGACATCCCTGCCAGCAGCAAGACCATTCAAGTGAACCTTCATGG
GCTAAACAGTACATTGAGTGAATTCTGAAGAAACATTAAAGGAAAAACAGTGGAAAAGT
ATATTAATCTGGAATCAGTGAAGAAACCAGGACCAACACCTCTTACTCATTATTCCCTTACA
TGCAGAATAGAGGCATTATGCAAATTGAACTGCAGGTTTCAGCATATACACAATGTCTT
GTGCAACAGAAAAACATGTTGGGAATATTCCCTCAGTGGAGAGTCGTTCTCATGCTGACGG
GGAGAACGAAAGTGACAGGGTTCTCATAAGTTGTATGAAATATCTCTACAAACCTCA
ATTAGTTCTACTCTACACTTCACTATCATCAACACTGAGACTATCCTGTCTCACCTACAAA
TGTGGAAACTTACATTGTTGATTTCACTGAGACTTTGTTTATTAAATTTTATTAGTG
TTAAGAATGCTAAATTATGTTCAATTATTCCAAATTCTATCTTGTATTTGTACAA
CAAAGTAATAAGGATGGTTGTACAAAAACAAACTATGCCCTCTTTTTCAATCACC
AGTAGTATTTTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTTTA
TTTTTTCAAGGAAAGATGGATTCAAATAATTCTGTTTGTAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSPHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNVKSVVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGLTLSASQ
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNMTLTCHEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNNSDKGLKVGEVFTV
DLGEAILFDPCSADSHPPNTYSWIRRTDNTTYIIKGPRLEVASEKVAQKTMDYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKSLPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRSPVASCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGGCGAAATGGCGCCCTCGGGAGTCTTGCAGTTCCCTGGCAGTCCTGGTGTGCTT
GCTTTGGGGTGCCCCTGGACGCACGGGCGGCGGAGCAACGTTCGCGTCATCACGGACGAGA
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTTATGCCCCGTGGTGCCCTGCT
TGTCAAAACTCTCAACCGGAATGGGAAAGTTGCTGAATGGGAGAAGATCTTGAGGTTAA
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTATCATAACTGCTC
TTCCTACTATTTATCATTGTAAGATGGTAATTAGGCCTATCAGGGTCCAAGGACTAAG
AAGGACTTCCATAAACTTATAAGTGATAAAAGAGTGGAAGAGTATTGAGCCCCTTCATCATG
GTTTGGTCCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTCAGCTATCTATGTGGA
TCAGGACGTGCCATAACTACTTATTGAAGACCTGGATTGCCAGTGTGGGATCATATACT
GTTTGCTTAGCAACTCTGTTCCGACTGTTATTAGGACTCTGTATGATATTGTGGC
AGATTGCCTTGTCCCTCAAAAGGCGCAGACCAAGCCATACCCATACCCCTCAAAAAAAAT
TATTATCAGAACTGCACAACCTTGAAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA
GATGTTCAGAAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTCCACAGAATGC
CATAAGACAACGCTCTGGTCCATCATTGCCACAGATAAAATCTAGTTAAATTTATAG
TTATCTTAAATTATTGATTGATAAAACAGAAGATTGATCATTGTTGGTTGAAGTG
AACTGTGACTTTTGAAATATTGCAGGGTTCACTAGATTGTCATTAATTGAAGAGTCTA
CATTCAGAACATAAAAGCACTAGGTATACAAGTTGAAATATGATTAAAGCACAGTATGATG
GTTTAAATAGTCTCTAATTGAAAAATCGTCCAAGCAATAAGATTATGTATATTGT
TTAATAATAACCTATTCAAGTCTGAGTTGAAAATTACATTCCCAAGTATTGATTGATT
TGAGGTATTAAAGAAGATTATTAGAGAAAAATTTCCTCATTTGATATAATTTCCTCTG
TTCACTGTGTGAAAAAAAGAAGATATTCCATAAAATGGAAAGTTGCCATTGTCTCAAG
AAATGTGTATTCACTGACAATTCTGTGGCTTTTAGAGGTATATTCCAAATTCCCTGT
ATTTTTAGGTTATGCAACTAATAAAACTACCTTACATTAAATTACAGTTCTACACA
TGGTAATACAGGATATGCTACTGATTAGGAAGTTTAAGTTCATGGTATTCTCTTGATTC
CAACAAAGTTGATTCTCTGTATTCTTACTTACTATGGTTACATTTTTATT
CAAATTGGATGATAATTCTGGAAACATTTTTATGTTTAGTAAACAGTATTGTTGTT
GTTTCAAACACTGAAGTTACTGAGAGATCCATCAAATTGAACAATCTGTTGTAATTAAATT
TTGCCCACTTTTCAGATTACATCATTCTGCTGAACCTCAACTGAAATTGTTTTT
TTTCTTTGGATGTGAAGGTGAACATTCTGATTGTTGCTGATGTGAAAAGCCTGGTA
TTTACATTGAAATTCAAAGAAGCTTAATATAAAAGTTGCATTCTACTCAGGAAAAG
CATCTTCTTGATATGCTTAAATGATTGTCCTCATACAGAAAGTTCTTAATTGAT
TTTACAGTCTGTAATGCTGATGTTAAAATAACATTATTAAAGACAA
ACTTCATATTCTGTGTTCTTCCTGACTGGTAATTGTTGTTGAGGATTCACAGGTA
AAGTCAGTAGGATGGAACATTAGTGTATTCTACTCCTAAAGAGCTAGAATACATAG
CACCTTAAAGAAGGGGAAAATCATAAAATACAATGAACACTGACCATTACGTAGTAGAC
AATTTCGTAATGCCCCCTTCTAGGCTCTGTTGCTGTTGAAATCCATTAGATTACAG
TATCGTAATATAACAGTTCTTAAAGCCCTCTCCTTAGAATTAAAATATTGTACCA
AAAGAGTTGGATGTGTAACTTGATGCCTAGAAAATATCCTAACGACAAAATAAC
TTCTAACCACTTCATTAAAGCTGAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIIFYAPWCPACQNL
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQPYPPSKLLSESAQPLKKVEEEQEADEEDVSE
EEAESKEGTNKDFPQNAIRQRSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

GCAGTGTCAGCTCGGAGACCGTATAATTGTTAACTAATTCAACAAACGGGACCCCTT
CTGTGTGCCAGAAACCGCAAGCAGTGTGACACTTCCCTCTGTGACCATGAAACTCTGGGTGTCTGC
AAGGTCTGGCCCAGAGCAGTGTGACACTTCCCTCTGTGACCATGAAACTCTGGGTGTCTGC
ATTGCTGATGGCCTGGTTGGTGTCTGAGCTGTGTGAGGGCAATTCTCACCTCTATTG
GGCACATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCAGTCTGAAAGAGTACATC
CTTGTGGAGGAAGCCAAGCTTCCAAGATTAAGAGCTGGCCAACAAAATGGAAGCCTGAC
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAAACTGG
TGAAGCGGCTAAACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGCAGGACTCAGCTGCA
GGTTTATGCCAACCTCTGTGAGCGGCAGTTCTTCCCCACTGATGAGGACGAGATAGG
AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTCCA
GAGGGAACTTCCAGGAACCAAGTACCAAGGCAATGCTGAGTGTGGATGACTGCTTGGATG
GGCCGCTGGCCTACAATGAAGGGACTATTATCATACGGTGTGGATGGAGCAGGTGCT
AAAGCAGCTTGATGCCGGGAGGAGGCCACCAACCAAGTCACAGGTGCTGGACTACCTCA
GCTATGCTGCTTCCAGTTGGGTGATCTGACCGTGCCTGGAGCTCACCGCCGCTGCTC
TCCCTGACCAAGCCACGAACGAGCTGGAGGAATCTGCGGTACTTGAGCAGTTATTGGA
GGAAGAGAGAGAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCCAGAAGGC
TCTATGAGAGGCCTGTGGACTACCTGCTGAGAGGGATGTTACGAGAGGCCTCTGTCGTGG
GAGGGTGTCAAACGACACCCCGTAGACAGAAGAGGCTTCTGTAGGTACCAACATGGCAA
CAGGGCCCCACAGCTGCTCATGCCCTTCAAAGAGGAGGACGAGTGGACAGCCGACA
TCGTCAAGTACTACGATGTCATGCTGATGAGGAATCGAGAGGATCAAGGAGATCGAAAA
CCTAAACTGCACGAGCCACCGTTGATCCCAAGACAGGAGTCCTCACTGTCGCCAGCTA
CCGGTTTCCAAAGCTCCTGGCTAGAGGAAGATGATGACCCCTGTTGTGGCCGAGTAAATC
GTCGGATGCAGCATATCACAGGTTAACAGTAAAGACTGCGAGATTGTTACAGGTTGCAAAT
TATGGAGTGGAGGACAGTATGAACCGCACTTCGACTTCTCTAGGCGACCTTGACAGCG
CCTAAAACAGAGGGAAATAGGTTAGCGACGTTCTTAACATGAGTGTAGAAGCTG
GTGGTGCACCGTCTCCCTGATCTGGGGCTGCAATTGGCTAAGAAGGGTACAGCTGTG
TTCTGGTACAACCTCTGGAGGGAAAGGTGACTACCGAACAGACATGCTGCC
TGTGCTTGTGGCTGCAAGTGGTCTCCAATAAGTGGTCCATGAACGAGGACAGGAGTTCT
TGAGACCTTGTGGATCAACAGAAGTTGACTGACATCCTTCTGTCCTTCCCTGTC
CTTCAGCCCATGTCAACGTGACAGACACCTTGTATGTTCTTGTATGTTCTATCAGGCT
GATTTGGAGAAATGAATGTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT
GTGACTGAAGTCCCAGCCCTCCATTCAAGCCTGTGCCATCCCTGGCCCAAGGCTAGGATCA
AAAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCTTGTACCTCAGGTGTT
TTAGGTGTGAGATGTTCAAGTAACAAAGTTCTGATACCTGTTACATGTTGTTTAT
GGCATTCTATCTATTGTGGCTTACCAAAAAATAAAATGTCCCTACCAAGAAAAAA

FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVVEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIANLSVQRQFFP
TDEDEIGAAKALMRLQDTYRLDPGTISRGELPGTKYQAMLSVDDCFGMGRSAYNEGDDYYHTV
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRLLSLDPSHERAGGNLR
YFEQLEEEEREKTLTNQTEAELATPEGIYERPVYLPERDVYESLCRGEVKLTPRQKRLF
CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYYDVMSEEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDPVVARVNRRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEDYR
TRHAACPVLVGCKWVSNKFHERGQEFLRPCGSTEVD

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTACTTCCTCCTTTAGTGGAAAGACAGACCATAATCCCAGTGTGAGTGAATTGATTGT
TTCATTTATTACCGTTTGGCTGGGGTTAGTTCGACACCTCACAGTTGAAGAGCAGGCAGAAGGAGTTGTGA
AGACAGGACAATCTTCTGGGATGCTGGCCTGGAAGCCAGCGGGCCTGCTCTGCTTTGGCCTCATTGACCC
CAGGTCTGGTTAAAAGCCTACTACTGGCCTGGTGCCATCAATCATTGATCCTGAGGCTGTGCC
CCTGGGCACCCACCTGGCAGGGCCTACCACCATTCGACTGAGCTCCCTGTTGGCTCTGCTGCGGCCAGCGCTTC
CCCTCATCTTAGGGCTGTCCTGGGTGCAGCCTGAGCCTCCTGCGGGTTTCTGGATCCAGGGGAGGGAGAAG
ATCCCTGTGTCAGGGCTGTAGGGGAGCGAGGAGGGCCACAGAATCCAGATTGAGAGCTCGCTAGACCAAAGTG
ATGAAGACTTCAAACCCCCGATTGTCCTCCTACTACAGGGACCCAAACAAGCCCTACAAGAAGGTGCTCAGGACTC
GGTACATCCAGACAGAGCTGGCTCCCGTGAGGGTTGCTGGCTGCTGACCTCCCGAGCTACACTGTCCA
CTTTGGCGTGGCTGTGAACCGTACGGTGGCCATCACTTCCCTCGGTTACTCTACTTCACTGGGAGCGGGGG
CCCGGGCTCCAGCAGGGATGCGAGGTGGTCTCATGGGATGAGCGGGCCCTGGCTCATGTCAGAGACCTGC
GCCACCTTACACACACTTTGGGCGACTACGACTGGTCTTCATCATGAGGATGACACATATGTGCAGGCC
CCCCGCTGGCAGCCCTGCTGGCACCTCAGCATCAACCAAGACCTGACTTAGGCCGGCAGAGGAGTTATTG
GCGCAGCGAGCAGGCCGGTACTGTCACTGGGCTTGGCTACCTGTTGTCAGGAGTCTCTGCTTCGTCTGC
GGCACATCTGGATGGCTGCGAGGAGACATTCTCAGTGCCTGCTGAGGATGACACATATGTGCAGGCC
ACTCTCTGGGCGTGGCTGTGTCACAGCACCAGGGCAGCAGTATGCTCATTTGAACGGCCAAAATAGGG
ACCTGAGAAGGAAGGGAGCTGGCTTCTGAGTGCCTTCGCGTGCACCCCTGCTCCGAAGGTACCGTCA
ACCGCCTCCACAAACGCTCAGCGCTCTGGAGTTGGAGGGCTTACAGTGAATAGAACAACTGCAGGCTCAGA
TCCGGAACCTGACCGTGCTGACCCCCGAAGGGGAGGCAGGGCTGAGCTGGCCCGTGGCTCCCTGCTCTTCA
CACACACCTCGCTTGAGGTGCTGGCTGGGACTACTTCACAGAGCAGCACACCTCTCTGTCAGATGGGG
CTCCAAGTGCCACTACAGGGGCTAGCAGGGCGACGGTGGATGCGTTGGAGACTGCCCTGGAGCAGCTCA
ATCGCGCTATCAGCCCCGCTGCGCTTCCAGAACAGCGACTGCTCAACGGCTATGGCGCTTCGACCCAGCAC
GGGCATGGAGTACACCCCTGGACCTGCTGTTGAATGTGTGACACAGCGTGGCACCGCGGGCCCTGGCTCGA
GGGTCACTGCTGCGGCCACTGAGCCGGTGGAAATCCTACCTATGCCCTATGTCACTGAGGCCACCGAGTGC
AGCTGGTGCTGCCACTCCTGGTGGCTGAAGCTGCTGCAAGCCCCGGTTCTCGAGGCGTTGCAAGCAATGTCC
TGGAGCCACGAGAACATGCAATTGCTACCCCTGTTGCTGGCTACGGGCCACGAGAACGGTGGCGTGGAGCTCCAG
ACCCATTCTGGGTGAAGGCTGCAAGCGAGCTTGAAGCGACGGTACCCCTGGGACGAGGCTGGCTGGCTCG
CTGTGCGAGCAGGCCCTTCCCAGGTGCAACTCATGGACGTTGCTCGAAGAACGACCCCTGTGGACACTCTCT
TCTTCTTACCCCGTGGACAAGGCCCTGGGCCAGTCTCAACCGCTGTCGATGAATGCCATCTGGCT
GGCAGGCCCTTCCAGTCCATTCCAGGACTCAATCTGCCCTGTCACCAACAGAGATCACCCCCAGGGCCCC
CGGGGCTGGCCCTGACCCCCCTCCCTGGCTGCTGACCCCTCCGGGGGCTCCTATAGGGGGAGATTG
ACCGCAGGCTCTGCGGAGGGCTGCTCTACAAACGCTGACTACCTGGCGCCGAGCCCGCTGGCAGGTGAAC
TGGCAGGCCAGGAAGAGGAGGAAGGCCCTGGAGGGCTGGAGGTGATGGATGTTCTCCGTTCTCAGGGCTCC
ACCTCTTCCGGCGTAGAGCCAGGGCTGGTGCAGAAGTCTCCCTGCGAGACTGCAGCCCACGGCTCAGTGAAG
AACTCTACCAACCGCTGCCCTCAGCAACCTGGAGGGCTAGGGGCCGTGCCAGCTGGCTATGGCTCTTTG
AGCAGGAGCAGCCAATAGCACTTAGCCCGCCTGGGGCCCTAACCTCATTACCTTCTGCTGCCTCAGCC
CCAGGAAGGGCAAGGCAAGATGGTGGACAGATAGAGAATTGTTGCTGTATTTTAAATATGAAAATGTTATTAA
ACATGTCTCTGCC

FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDCSRRLD
QSDEDFKPRIVPYYRDPNPKVVKLTRYIQTELGSRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVVSQHDERPAWLMSETLRHLHTFGADYDWFFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLRSLLRLRPHLDGCRG
DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPGEAGLSPVGLPAPFTPNSRFEV
LGWDYFTEQHTFSCADGAPKCPQLQGASRADVGALETALEQLNRQYQPRLRFQKQRLLNGYR
RFDPARGMETLDLLCCTQRGHRRALARRVSSLRPLSVEILPMPYVTEATRVQLVPL
VAEAAAAPAFLEAFAANVLEPREHALLTLLVYGPREGGRGAPDPFLGVKAAAELERRYPG
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTWTRPGPEVLRNCRMNAISGWQAFFP
VHFQEFNPALSPQRSPPGPPGAGPDPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA
RARLAGELAGQEEEAELEGLEVMDVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGLGGRALAMALFEQEQANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGCACCGTGGAAACGTGAGAGGAAACCGTGCACCGTGCCTTCTGTCCCCAAGCC
GTTCTAGACGCGGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTGATGCTTGG
AAGCATTCTGTGCTTGTACACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCTAACAAAGAAGATATCTGAAAATTC
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTCGAGTATACTGTATTATCCTGTAAAACC
CAAAGATGTGAGTCTTGGGCTGCAGTAAGGAGACTTGGACCAAACACTGTGACAAAGCAG
AGTTCTCAGTTCTGAAATGTTAAAGTGTGAGTCATTAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCCTTGATAAGTATAGAGACCAATACA
GTTCTCCTGCACGCCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGCAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTAATACCAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTACCA
CAACCAGGTAGTAGAAGGCTGTTGTCAGATATGGCTTACTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGTATGGGTATACGCCCTAGGGCATTTGGCATATTTCAAT
GATGCATTGGTTTCTTACCTCAAATGGTCTGACAATGACTTGAGAAGTGGTAGAAAAGCG
TGAATATGATCTTGTATAGGACGTGTGTCATTATTGTTAGTGTAACTACATATCCAA
TACAGCTGTATGTTCTTTCTTAATTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTAAATGAGGGTGGTTTTCTTAAAACACATGAACATTGAAATG
TGTGGAAAGTGTGTTAAGAATAATAATTGCAAATAAACTATTAATAATATTATAT
GTGATAAATTCTAAATTGAAACATTAGAAATCTGTGGGCACATATTGCTGATTGGTT
AAAAAATTAAACAGGTCTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAAACCTTGTGTTCCCTTACTTCTAATACTGATTATGTTCT
AAGCCTCCCCAAGTTCCAATGGATTGCCCTCTCAAAATGTACAACTAAGCAACTAAAGAAA
ATTAAAGTGAAGTTGAAAAT

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAEFFSSENVKFESINMDTNDMWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHТИKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

FIGURE 122

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSCNYGGSVKNCCPLNWEYFQSSCYFFSTDТИSWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPPNNIATLEDCATMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCCCTCAGCAACCCCTGACATGGCGCTGAGGCGGCCACCGCGAC
TCCGGCTCTGCCTCGGCTGCCTGACTTCTTCCTGCTGCTGCTTTCAGGGGCTGCCTGATAGGGGCTGTAATC
TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTGAAAGTGTGAACTGTCCTGCATCATTACGGATTGC
AGACAAGTACCCCCAGGATCGAGTGGAAAGAAAATTCAAGATGAACAAACACATATGTGTTTTGACAACAAAA
TTCAGGGAGACTTGGCGGCTCGTGCAGAAATACTGGGAAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTATCGCTGTGAGGTGCTGCTGAAATGACCGCAAGGAAATTGATGAGATTGTGATCCAGTTAA
CTGTCAGTGAAGCCAGTGACCCCTGCTGTAGAGTGCAGAAGGCTGTACCACTAGGCAAGATGGCAACACTGC
ACTGCCAGGAGACTGAGGGCCACCCCCGGCTCACTACAGCTGCTGCATGATGTACCACTGCCACGGATT
CCAGAGCCAATCCCAGATTTCGAATTCTCTTCCACTTAAACTCTGAAACAGGACTTTGGTGTCACTGCTG
TTCAAGGACGACTTGGCAGTACTACTGCATTGCTTCAATGACCGCAGGCTCAGCCAGGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTGGCGAAATTGGGGGTTCTGGTTGCTGTACTGCCCTGA
TCACGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTCATCAACAAATAACAGGATGGAGAAAGTTACAAGA
ACCCAGGGAAACCAAGATGGAGTTAACATACATCCGCACTGACGAGGAGGGCAGTCAGACACAAAGTCATGTTG
TGATCTGAGACCCCGGGTGGCTGAGAGCGCACAGAGCAGCAGTGCACATACCTCTGCTAGAAACTCCTGTCAA
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTAGAAGCTTTGCTTGGCCAAAGGTTGACCA
CTACTCTTCTTACTCTAACAGCCACATGAATAGAAGAATTTCCTCAAGATGGACCCGGTAAATATAACCACAA
GGAAGCAGAAACTGGGTGCGTTCACTGAGTTGGGTTCTAACATGTTCTGGCTGATTCCCGCATGAGTATTAGG
GTGATCTTAAAGAGTTGCTCACGTAACGCCCGTGTGGGCTGAGGCAAGCAGCATGTTACCAACTGGTCGTT
CAGCAGCCACGACAGCACCATGTGAGATGGCAGGTGGCTGGACAGCACCCAGCAGCGATCCGGCGGAACCCA
GAAAAGGCTTCTTACACAGCAGCCTTACTTCATCGGCCCACAGACACCACCGCAGTTCTTAAAGGCTCTGC
TGATCGGTGTTGCACTGTCATTGTGGAGAAGCTTTGGATCAGCATTGTAAGGAAACCAACAAATCAGGAAG
GTAAATTGGGTGCTGGAAGAGGGATCTGCTGAGGAACCTGCTTGTCCAACAGGGTGTCAAGGATTTAAGGAAA
ACCTTCGTCTTAGGCTAACAGTCTGAAATGGTACTGAAATATGCTTTCTATGGGTCTTGTATTAAAGGCTCTGC
TACATCTAAATTGGTCTAACAGGATGTATTTGATTATTGAAAAGAAATTCTATTTAAACTGTAATATATTGT
CATACAAATGTTAAATAACCTATTTTAAAGGTTCAACTAACGGTAGAAGTCAAGCTACTAGTGTAAAT
TGGAAAATATCAATAATTAGAGTATTTACCAAGGAATCCTCTCATGGAAGTTACTGTGATGTTCTTTCT
CACACAAGTTAGCCTTTCAAAAGGAACCTACATCTGTCACACATCAGACCATAGTTGCTTAGGAAACCTT
TAAAATTCAGCTAACAGCAATGTTGAAATCAGTTGCTCTCTTCAAAAGAAACCTCTCAGGTTAGCTTGAACCT
GCCTCTCTGAGATGACTAGGACACTGCTACCCAGGGCCACCCAGAAGCCCTCAGATGTACATACACAGATG
CCAGTCAGCTCTGGGGTTCGGCCAGGGCCCCCGCTAGCTCACTGTCCTCGCTGCTGCCAGGAGGCCCT
GCCATCCTGGGGCTGGCAGTGGCTGTGCTCCAGTGGCTTACTCACGTTGGCCCTGCTCATCCAGCACAGC
TCTCAGGTGGGACTGCAGGGACACTGGTGTCTCCATGTCAGCTGCCAGCTTGGCTCTGTAACAGACCTCT
TTTGGTTATGGATGGCTCACAAATAGGGCCCCAATGCTATTTTTAAGTTGTTAATTATTGTT
AAGATTGCTAACAGGCAATTGCAAGTGTCAAGTACAATAACATTAAAGAAATGGAT
CCCACGTGCTCTTGGCCACAGAGAAAGCACCCAGCAGCCACAGGGCTCTGCGCATTTCAAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGCCTTTAAAGAACGTCAGGTGGAGCAGCCAGGTGAAAGGCCCTGGGGAGGAAAG
TGAAACGCCCTGAATCAAAAGCAGTTCTAATTGACTTAAATTTTCACTGCCGGAGACACTGCTCCATT
TGTGGGGGACATTGCAACATCACTCAGAAGCCTGTTCTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT
GCCGTGCTGGACTCAGGACTGAAGTGTGAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTCCTGGA
GAATGGCTCTCAACTCACCTTGTCTTCAGCTTCAAGTGTCTGGTTTTTATACCTTGTACAGCTTTTTT
AATTGCTACATGAGACTGTGTTGACTTTTTAGTTATGAAACACTTGCCTCAGGCGCTGGCAGAGGCA
GGAAATGCTCCAGCAGTGGCTCAGTGTCTCCCTGGTGTCTGCATGGCATCTGGATGCTTAGCATGCAAGTTC
CCTCCATCATTGCCACCTGGTAGAGAGGGATGGCTCCCCACCCCTCAGCGTTGGGATTCAAGCTCCAGCCTCCT
TCTTGGTTGTCATAGTGTAGGGTAGCCATTGCCCCCTTCTTAAACCTTACACTAGTGCCTA
TGGGAACCCAGGCTGAAAAAGTAGAGAGAAGTGAAGTAGCTGGGAAGTAGCTGCTTAAACTGAGACTAGA
CGGAAAAGGAATACTCGTGTATTAAAGATATGAAATGTGACTCAAGACTCGAGGGCGATACGAGGCTGTGATTCT
GCCCTTGGATGGATGTTGCTGTACACAGATGCTACAGACTGTACTAACACACCGTAATTGGCATTGTTAAC
CTCATTATAAAAGCTCAAAAAACCCA

FIGURE 124

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLSKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267